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Best Local Similarity
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SIGNAL
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Matches
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09DFY8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QNWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
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Rama catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordato, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura, Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catebbelana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENOAPVHFVGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242552.
EMBL, AF242525.
EMBL, 28-JUJ-02.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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                                                                                                                                                                                                                                                                                       Rana pipiens (Northern leopard frog).
                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000535; RNaseA; 1.
                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
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                                                                                                                                                                                                                              Onconase precursor
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                          1 ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                               24 QDWATFKKKHLTDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79
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EMBL; AF242553; AAG31439.1; --
DDB; 1MSB; 09-JAN-03.
GO; GO:0003467; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHBLPVHFAGVGICP 129
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 VLSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
                                                                                                                                                                                                                                                                                                                    10;
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%; Score 225.5; DB 13; Length 128; 39.3%; Pred. No. 4.1e-18;
                                                                                                                                                                                                                                                          40.5%; Score 243; DB 13; Length 129; 42.5%; Pred. No. 4e-20; tive 25; Mismatches 30; Indels 10
                                                                                                                                                                                                                                                                                   4e-20;
~hes 30; Indels
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                                                                                                                                              1 23 POTENTIAL.
24 129 RC-RNASE4 RIBONUCLEASE.
129 AA; 14724 MW; 826A62882B10ABDA CRC64;
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989719CF52053ECC CRC64;
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01-0CT-2003 (TIEMBLIEL 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana castesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Prec. w..
tive 21; Mismatches
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DFY8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
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298SM1;

098SM1

RESULT 5

Q98SM

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127
                                                                                                                                                      POTENTIAL.
                                                            Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                   132 R
14625 MW;
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ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                    72; Conservative
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22
132 AA;
 P11916; 1BC4.
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Best Local 8
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 HSSP;
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DAR REPRESENTATIONS SOLVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNSNV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                             MEDLINE=21539506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; "Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.";
                                                                                                                                            RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC-RNasell ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=2051555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 LSTTRPQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.1%; Score 444.5; DB 13; Length 77.3%; Pred. No. 2.6e-43; ive 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                             J. Mol. Evol...

EMBL; AF351208; AAK30254.1; -..

EMBL; AF351208; AAK30254.1; -..

EMSP; P11916; IBC4.

GO; GO:0004522; F:nucleic acid binding; IEA.

GO; GO:0004522; F:nucleic acid binding; IEA.

InterPro; IPR001427; RNaseA.

PETAM; PF00074; TRASEA; 1.

PROM; PD000535; RNaseA; 1.

SWART; SM00092; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95D61760F729868E CRC64;
                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28:4097-4104(2000).
                                                                                              (TrEMBLrel. 17, Created)
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 PH
14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.3
Matches 85; Conservative
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 132 AA;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
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                                                                                                                                                                                                                 NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                          01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Signal.

SIGNAL

Q9DF78;

ID DDT ACCOOC OCCOOC OCOOC OCCOOC OCO

09DF78

RESULT 6

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22 ONWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure.";
Nucleic Acids Rea. 28:2375-2382(2000).
EMBL; AF165133; AAF76935.1; -.
PIR; A39035; A39035.
HSSP; P22069; IONC.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
Onconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Rana.
N.131_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 VLITSEFYLSDC---NVTSRPCKYKKKSTNIFCYTCENQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                             RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 23 POTENTIAL.
127 Aa; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           62.0%; Score 372; DB 13; 64.9%; Pred. No. 5.8e-35; tive 10; Mismatches 27.
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Gaps

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82

Q98SM2;

098SM2

RESULT 2 298SM2

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23 QNWATFQQKHITNTSSINCSNIMMNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV
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MEDIINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
BENBL; AF51211; AAK30257.1; -.
HSSP; P11916; 18C4.
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).

GEMBL, AF351210; AAK30256.1;
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stana catesbelana (Bull Irog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LSSTKFQLDICTRIFITPRFCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 LSTTRFQLNTCTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.1%; Score 474.5; DB 13; Length 133; 77.5%; Pred. No. 9.2e-47; Live 12; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.9%; Score 467.5; DB 13; Length 133; 75.7%; Pred. No. 5.9e-46; Live 14; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LSSIKFOLDICTRIFITPRPCPYSSRTETNYICVKCENOYPVHFAGIGOCP
                                                                                                                                                                                                                                   GO: GO:0003576; F:nucleic acid binding; IEA.
GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Propor; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PC; 1.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA, 1.
Probom; PD000535; RNaseA. 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C8785B236B26E54E CRC64;
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133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-07-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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133 AA; 14615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21539506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; "Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana
                                                                                    LSTTRFQLNTCTRISITPRPCPYSSRTENNYICVKCENOYPVHFAGIGRCP 133
                                                                                                                                                                                                                                                                                                                                                                                          01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                          LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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82.7%; Pred. No. 8.4e-48;
tive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AR551207; AAK30253.1; -.
EMBL, AF3595973; AAL87036.1; -.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Prodom; PD000532; RNaseA; 1.
SMART; SM00922; RNASE Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RC-RNASE7.
131A745187978687 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                               132 AA.
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(TrEMBLrel. 17, Last seq
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MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Mol. Evol. 53:31-38(2001).
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Best Local Similarity
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01-JUN-2001
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1 QNWATFQQKHIINTBIICNT.....ICVKCENQYPVHFAGIGRCP 110
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                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Description	Q98sm0 rana catesb	rana	Q98s18 rana catesb	Q98sml rana catesb		Q9i8v8 rana pipien	rana		Q9dfy8 rana catesb		09dfys rana catesb	Q9w738 xenopus lae	O9bec1 traquîus ja	Q80z85 mus musculu	Q80xs4 mus musculu
SUMMARIES	Q98SM0	Q98SL9	Q98SL8	Q98SM1	Q9DF78	Q918V8	QBUVX5	Q9DFY6	Q9DFY8	Q9DFY7	Q9DFY5	Q9W738	Q9BEC1	Q80Z85	Q80XS4
DB	133	13	13	13	13	13	13	13	13	13	13	13	9	11	11
% Query Match Length DB	133	133	133	132	132	127	127	129	128	128	128	169	170	144	153
% Query Match	92.4	79.1	77.9	74.1	62.0	46.2	45.6	40.5	37.6	37.2	35.8	26.8	21.3	21.2	21.2
Score	554.5	474.5	467.5	444.5	372	277.5	273.5	243	225.5	223.5	214.5	191	128	127.5	127.5
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Q7yrj6 balaena mys Q861y5 colobus gue Q9tvC0 sus scrofa Q8vd94 berylmys bo Q8vd89 rattus norv Q9bh14 antilocapra Q7yrj5 tursiops tr Q8k2t2 mus musculu Q8c53 mus musculu Q8c1y1 pygathrix r Q8c6y2 mus musculu Q8c6y2 mus musculu Q8c6y2 mus musculu Q8c6y2 pygathrix r Q8c6y2 mus musculu Q8c6y2 bygathrix r Q8c6y2 mus musculu Q8c6b bygathrix r Q8c6b mus musculu Q8c6b tragulus ja Q8vd89 rattus tiom Q8vd95 tragulus ja Q8vd84 rattus tiom Q8vd95 berylmys bo Q9bec2 tragulus ja Q9vd84 rattus tiom Q8vd86 saguinus oe Q8vd86 saguinus oe Q8sq06 sateles geof Q9bec3 tragulus ja	ostomi; e; Rana. from the	s 5; Indels 1; Gaps 1;
147 6 Q7YRJ6 146 6 Q861Y5 156 1 Q8TUCO 150 11 Q8VD84 150 11 Q8VD84 144 6 Q7RJ14 147 6 Q7RJ2 149 11 Q8KZT2 149 11 Q8KZT2 149 11 Q8KZT2 146 6 Q861Y3 146 6 Q861Y3 146 6 Q861Y3 146 6 Q861Y3 146 6 Q861Y3 146 6 Q861Y3 147 6 Q8EDB9 148 11 Q8CCB4 148 11 Q8CCB4 149 11 Q8CCB4 140 Q8DB9 156 6 Q8SQOB 156 6 Q8SQOB 156 6 Q8SQOB 156 6 Q8SQOB 156 6 Q8SQOB 157 6 Q8BCG	ALIGNMENT PRT; 133 reated) ast sequenc ast annotat O8 precurso Craniata; eobatrachia 3320; o YD., Dy se A superf a binding; ribonucleas ribonucleas 87FCF122C Score 554.5 Pred. No. 5	2, Mismatche
17 123.5 20.6 18 122.5 20.3 20 121.5 20.2 21 121.5 20.2 22 118.5 19.8 24 118.5 19.4 25 116.5 19.4 26 16.5 19.4 27 116.5 19.4 28 116.5 19.4 29 116.5 19.3 30 115 19.2 31 113.5 19.2 34 100.5 18.2 35 109.5 18.2 36 109.5 18.2 37 109.5 18.2 38 100.5 18.2 39 100.5 18.2 40 100.5 18.1 42 107.5 17.9 44 107.5 17.6	PRELIN D1 (TrEME D1 (TrEME D3 (TrEME D3 (TrEME D3 (TrEME D3 (TrEME D3 (TrEME D3 (TrEME D4	Matches 103; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 CKNGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKYIIVACEGTPSVPVHFDGS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <1 19 POTENTIAL.
20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;</pre>
                                                                                                                                                                                                                                                      Tragulus javanicus (Lesser Malay chevrotain).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Tragulina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Tragulus javanicus)...;

Eur. J. Biochem. 268:3890-3897(2001).

-1. SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

HSSP, P00656; 1LSQ.

GO; GO:0004519; F:endonuclease activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; Ribancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A., Warmels H.W., Beintema J.J.; "Secretory ribonucleases in the primitive ruminant chevrotain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.6%; Score 131; DB 6; Length 170; ilarity 33.1%; Pred. No. 2.9e-07; Conservative 17; Mismatches 46; Indels
                                                                                                                                                                                                  Brain-type ribonuclease ribonuclease precursor (Fragment).
                                                                                                       01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
                                                            170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; I.
PRINTS; PR00794; RIBONUCIEASE.
PPCDOOM: PD000535; RNaseA; I.
SWART; SM00092; RNASE_PC; I.
PROSITE; PS00127; RNASE_PANCRAATIC; I.
BRIGONUCIease; Hydrolase; Nuclease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21347458; PubMed=11453981;
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MEDLINE=22493143; PubMed=12548285;
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                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Tragulidae, Tragulus.
NCBI_TaxID=9849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 AVLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 GRCP 111
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ANG4.
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                                                                                                                                                                                                                                    RNASE B.
Q9BEC1
Q9BEC1
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Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.; "Angiogenins: a new class of microbicidal proteins involved in innate immunity.";
                                                                                                                                                                                                                        34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITP-RPCPYSSRTE
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     5,
                                                                                                                                                                          21.2%; Score 128.5; DB 11; Length 144; 38.2%; Pred. No. 4.7e-07; ive 13; Mismatches 29; Indels 5;
                                         7, 2004, 21:46:04
                                    Nat. Immunol. 4:269-273 (2003).
                                                                                                                                                                                                                                                                      89 TNYICVKCENQYPVHF 104
                                                                                                                                                                                                                                                                                            122 FRYIVIACEDGWPVHF 137
                                                                                                                                                                                                 29; Conservative
                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                   Matches
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                                                                                               SEQUENCE
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SIGNAL
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                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                             24 ÓDWETFÓKKHLTDTKKVKCDVEMAKALF----DCKKTNTFIYALPGRVKALCKNIRDNTD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AG31442.2; -.
HSSP; P22069; 10NC.
                                                                                                                                                                                                                                                                                                                                                                                    9; Gaps
                                                                   RC-RNase3 ribonuclease precursor.

Rana catesbeiana (Bull frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;

MEDLINE-25512555; PubMed-11058105;
Liao Y.D., Hang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Ruang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                       GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                             128 RC-RNASE3 RIBONUCLEASE.
14517 MW; 2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2001 (TrEMBirel. 16, Created)
01-OCT-2001 (TrEMBirel. 18, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             37.3%; Score 226.5; DB 13
41.1%; Pred. No. 1.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
                     128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                          catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
EMBL; AF242554; AAG31440.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                    46; Conservative
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       128 AA;
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                          SEQUENCE FROM N.A.
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                                         01-MAR-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                          Signal.
                                 Q9DFY7;
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                     Q9DFY7
                                                                                                                                                                                                                                                                                                                               CHAIN
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Q9DFY5
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONWATFOOKHII--NTPIICN-TIMDNNIYIVGGOCKRVNTFI-ISSATTVKAICTGVIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; cell 83:621-630(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Cranīata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 MN-VLSTTRFQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        œ
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                                                                                                                                                                                                                                                                                                              35.8%; Score 217.5; DB 13; Length 128; 39.3%; Pred. No. 1.7e-17;
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                                                                                                                                                                                                                                                                                                                                                                  40; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AFL59166; AAD41901.1; --
HSSP; P00656; 1LSQ.
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GO; GO:0004522; F.pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                               1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
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39.3%; Pred. No. 5.3e-11;
iive 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96069863; PubMed=7585965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00074; rnaseA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Local Similarity
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                              Conservative
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                                                                                                                           24 1
129 AA;
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128 AA;
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                                                                                                                                                                                                                              49;
                                                                                                                                              SEQUENCE
                                                                                                                                                                                      Query Match
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                                                                                        Signal.
                                                                                                          SIGNAL
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                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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        RARRETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF242555, AAG31441.2; -.

EMBL, AF242555, AAG31441.2; -.

EDB; IKVZ; 28-UUL-02.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Gaps
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordača, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog) ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%; Score 277.5; DB 13; Length
49.5%; Pred. No. 1.7e-24;
iive 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                  "Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332139; AAL54383.1;
PIR; A39035, A39035.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953F90D351CFEEF3 CRC64;
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. C. Created)
01-0XF-2001 (TrEMBLrel. 16, Created)
01-0XT-2001 (TrEMBLrel. 18, Last sequence update)
10-0XT-2003 (TrEMBLrel. 18, Last annotation update)
RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                       127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                             Rana pipiens (Northern leopard frog)
                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
SEQUENCE 127 AA; 14469 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55; Conservative
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                   Liao Y.-D., Wang S.-C.;
                                                                                                                                          Onconase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                    NCBI_TaxID=8404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver
                                                                             01-MAR-2002
                                                                                                                   01-OCT-2003
                                                                                                  01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                       Q8UVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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RESULT 8
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              Serves

ACCOMPANCE

OR ACCOMPANCE

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                                                                                                                                                                                                                                                                                                                                      ONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN 59
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EMBL; AF242553, AAG31439.1; -.
PDB; 1M58; 09-JAN.03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGICP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RC-RNASSZ ribonucleaser z.j. mast annotation upuate, RC-RNASSZ ribonuclease precursor. Rana catesbeiana (Bull frog). Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana. NCBI_TaxID=8400;
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MEDLINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
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                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7e-19;
7e-19;
7hes 38; Indels
                                                                                                                              RC-RNASE4 RIBONUCLEASE.
826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA.
                                                                                                         POTENTIAL.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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ProDom, PD000535, RNaseA, 1.
PROSITE, PS00127, RNASE_PANCREATIC, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                      14724 MW;
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NCBI TaxID=8404;
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                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                  Q9I8VB;
                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                     0918VB
                                                                                                  Signal
                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                          Q9I8VB
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DR REPRESENTATION SOLVER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
Liao Y.-D., Hung H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVXAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF351208; AAK30254.1; -.
                                                                      61-JUN'2001 (TrEMBLrel. 17, Created)
01-JUN'2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
RNase A-type ribonuclease rc204 precursor.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RusseA.
Ffam; PF00074; rnaseA: 1.
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
95D61760F729868E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            73.9%; Score 448.5; DB 13; 78.2%; Pred. No. 2.1e-44; Live 7; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AA
                                                 132 AA
                                                                                                                                                                                                                                                                                                                                         Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                 PRT;
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01-OCT-2003 (TrEMBLrel. 25, Last at
RC-Rasell ribonuclease precursor.
Rana catesbelana (Bull frog).
                                                                                                                                                                                                  MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                    132 AA; 14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.9
Best Local Similarity 78.2
Matches 86; Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bullfrog)
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                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                               Q98SM1;
                                                                                                                                                                                                                                                                                                                                                                                Signal.
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                                                Q98SM1
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                       RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                     2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALSOURE 20330357; PubMed=10871370; Maizel J.V. Jr., Rybak S.M.; Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; Chen S.-L., De Cific mRNA encoding a cytotoxic ribonuclease contains a J. UTR of unusual length and structure."; Nucleic Acids Res. 28:2375-2382(2000).

BMBL, AF165131, AAF76935.1; ---
PIK, A39035; A39035.
HSSP; P22069; LONC.
GO, GO:0003676; Finucleic acid binding; IBA.
GO, GO:0004522; Fipancreatic ribonuclease activity; IEA.
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Rana pipins (Northern leopard frog.).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 ELSTISFKLNTCIRDSIIPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132
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                                                                                                                                                                                                                                                                                                                             Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                   27; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRN01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PF0000; PD000535; RNaseA; 1.
SMART; SM00922; RNASe Pc; 1.
PROSIIE; PS00127; RNASE_PROREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                  POTENTIAL.
RC-RNASEL1 RIBONUCLEASE.
DBD9AS17452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                        Score 376; DB 13;
Pred. No. 5.9e-36;
9; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.4%; Score 281.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
Probom, PD000535; RnaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNAŠE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA; 14491 MW;
                                                                                                                                                                                                                                               132 R
14625 MW;
                                                                                                                                                                                                                                                                                                                          61.9%;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Local Similarity
Society
T3; Conservative
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132 AA;
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Gaps

111

Q98SM2

RESULT 2

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Q98SM2

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2 ONWAIFQOKHIINTPII-CNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 QNWATFOEQHITNTSSINCSNIMNNSLYIVGGOCKKVNTFIASSATTVKGICSGVTDKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
BEMEL, AF351211; AR30257.1; -.
HSSP; P11916; LBC4.
GO; GO:0003576; F:nucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).

J. Mol. Evol. 53:51210;

J. AAK30256.1;
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNase A-type ribonuclease rc218 precursor.

Fana catesbeiana (Bull frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.7%; Score 471.5; DB 13; Length 133; 76.6%; Pred. No. 4.4e-47; Live 13; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                         78.8%; Score 478.5; DB 13; Length 133; 78.4%; Pred. No. 6.7e-48; tive 11; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LSTTRFQLNTCTRTSITPRPCPYSSRTBTNYICVKCENQYPVHFAGIGRCP
                                                                                                                 GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                   C8785B236B26E54E CRC64;
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133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133
                                                                                                                                                                                              Prodom; PD000535; RNASEA; 1.
SMART; SM00092; RNASE_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00074; rnaseA; 1.
ProDom, PD000535; RNaseA; 1.
SMART; SMO0092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                                                                                                                                              22 PU
14615 MW;
                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 78.4 Matches 87; Conservative
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85; Conservative
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133 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; "Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordača, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                         LSTTRFOLNTCTRTSTTPRPCPYSSRTENNYICVKCENOYPVHFAGIGRCP 133
                    LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LSTTRFQLNTCTRISITPRPCPYSSRTBTNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.3%; Score 487.5; DB 13; Length
83.6%; Pred. No. 5.9e-49;
ive 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAR30253.1; -.
EMBL; AF3559578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                             132 AA
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Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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MEDLINE=21539506; PubMed=11683320;
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132 AA; 14412 MW;
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92; Conservative
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132
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Liver;
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                    61
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Signal

CHAIN

Matches

RESULT 3

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9 82

Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2004, 21:29:10; Search time 31.566 Seconds (without alignments) 1109.503 Million cell updates/sec Run on:

US-09-961-400-17 607 Title: Perfect score:

1 MONWAIFQOKHIINIPIICN.....ICVKCENQYPVHFAGIGRCP 111 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
4: sp_tungi:*
5: sp_tungi:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_phage:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_virus:*
15: sp_virus:*
15: sp_virus:*
16: sp_virus:*
17: sp_virus:*
18: sp_virus:*
18: sp_virus:*
19: sp_virus:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		ion	rana catesb	rana	rana	rana	rana catesb	rana catesb	rana pipien	rana pipien	rana catesb	rana catesb	rana catesb	rana catesb	xenopus lae	raquîus ja	080z85 mus musculu	mus musculu
מ		Description	0ms860	098sm2	098819	098818	098sm1	09df78	091878	Qanvx5	09dfy6	09dfy8	09dfy7	09dfy5	09w738	Ogbec1 t	080285	Q80xs4
SUMMAKIES		ID	0888Q	Q98SM2	61886Q	81S860	Q98SM1	Q9DF78	878160	QBUVX5	Q9DFY6	Q9DFY8	Q9DFY7	Q9DFY5	Q9W738	Q9BEC1	Q80Z85	Q80XS4
		DB	13	13	13	13	13	13	13	13	13	13	13	13	13	G	11	11
		Length	133	132	133	133	132	132	127	127	129	128	128	128	169	170	144	153
	ж	Query core Match Length DB I	92.3	80.3	78.8	77.7	73.9	61.9	46.4	45.7	40.5	37.8	37.3	35.8	26.9	21.6	21.2	21.2
		Score	560.5	487.5	478.5	471.5	448.5	376	281.5	277.5	246	229.5	226.5	217.5	163	131	128.5	128.5
	,	Result No.		7	т	4	2	9	7	8	60	10	11	12	13	14	15	16

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44 60	M W M	Q86.1y2 pygathrix b Q86.1y1 pygathrix a Q8vd89 rattus norv Q95ne6 bubalus bub Q8c7e4 mus musculu Q8vd95 berylmys bo Q8bdb9 tragulus ja Q8vd84 rattus tiom	Q8eq05 lagothrix l Q8e663 mus musculu Q2tv28 eulemur ful Q9tv30 saguinus oe Q2bec3 tragulus ja Q8eq06 ateles geof Q2bec2 tragulus ja Q8eq08 saimiri sci
.0 147 6 .8 150 11 .7 163 6 .5 116 6	2.2 144 6 .9 147 6 .9 149 11 .9 149 11 .8 150 11 .7 146 6	19.5 146 6 Q86172 19.2 152 11 Q8VD89 18.9 124 6 Q9SNE 18.5 148 11 Q8C7E4 18.5 149 11 Q8VD95 18.5 149 11 Q8VD95 18.5 152 11 Q8VD84	156 6 0 148 11 119 6 0 1119 6 0 142 6 0 156 6 0 156 6 0
7 8 6 0 1	22 122.5 23 121.5 24 120.5 25 120.5 26 120.5 27 120 28 110.5	111111111111111111111111111111111111111	111 110 110 110 109 109 108

ALIGNMENTS

9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 SQW--FATQHITITANPQCNVEMLPINRNRTRCKNINTFLHTHFANVVGVCGNPSGLCSN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                   A menuina=2.024979; Vendent=10.79180;
A fandy J., Dyer K.D., Rosenberg H.F.;
Teamily by rapid gene sorting and positive selection.";
Froc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
R MSD; P10153; HHZ.
R MSD; P10153; HHZ.
R GO; GO:0003676; F:mucleic acid binding; IEA.
R GO; GO:0004522; F:mucleic acid binding; IEA.
R GO; GO:0004522; F:mucleic acid binding; IEA.
R ThterPro; IRR01427; RNaseA.
R PRINTS; PR001747; RNaseA.
R PRINTS; PR00194; RIBONUCLEASE.
R PRODOS PROSS PRASE PC: 1.
R PROSITE; SR001927; RNASE PC: 1.
R PROSITE; PS00127; RNASE PC: 1.
R PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Gaps
                                                                                                                                   Mus saxicola (Spiny mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang J., Dyer K.D., Rosenberg H.F.,
Zhang J., Dyer K.D., Rosenberg H.F.,
"Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.",
Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706 (2000).
BEMBI, ARF318394, AAF67694.1; -.
HSSP, PIOIS3; HHZ.
GO, GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.9%; Score 133; DB 11; Length 152; 30.3%; Pred. No. 2e-07; live 19; Mismatches 42; Indels 24
                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Eosinophil-associated ribonuclease 10.
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Last annotation update)
                       152 AA
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01-0CT-2000 (TrEMBLrel. 15, Last seque:
01-0CT-2003 (TrEMBLrel. 25, Last annot:
Eosinophil-associated ribonuclease 44.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20243759; PubMed=10758160;
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                  PRELIMINARY;
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                                                  Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;
                                                                                                                                            22.5%; Score 131; DB 11; 30.6%; Pred. No. 3.5e-07; iive 20; Mismatches 37;
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288642.3 AG30414.2; -.
HSSP; P11916; 1864.
GO; GO:0003676; F:nucleic acid binding; IEA.
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MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of Rhase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Bvol. 53:11318(2001).
BENBL; AF351208; AAK30254.1;
HSSP; P11916; 1BC4.
GO, GO:0003566; Finucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
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Ranidae; Rana.
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
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48.2%; Pred. No. 7.2e-24;
Live 14; Mismatches 35; Indels
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95D61760F729868E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CUT-2003 (TrEMBLrel. 25, Last annotation update)
Nose A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Mercazoa; Chordata; Craniata; Vertebrata; Bapahibia; Barrachia; Annora; Nechordata; Neobatrachia; Ranoidea; NCBI_TAXID=8400;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasell ribonuclease precursor.
Rana catesbeiana (Bull frog).
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SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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132 AA; 14704 MW;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                            23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
                                                                                                                                                                                                                                                                                                                                                                         3 DWLTFQKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 FOKKHLINT-RDVDCN-----NIMSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96069863; PubMed=7585965; Kinoshita N., Minshull J., Kirschner M.W.; Kinoshita N., Minshull J., Kirschner M.W.; "The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 169;
                                                                                                                                                                                                                                                                              DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 LTTSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.1%; Score 157.5; DB 13; Length 36.1%; Pred. No. 3.3e-10; ive 19; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinoshita N., Kirschner M.W.;
Submitted (UUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF159166; AAD41901.1; -.
HSSP; P00656; ILSQ.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR001427; RNaseA.
PF00074; rnaseA; 1.
GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Product Products: RNASEA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18851 MW; D969F3E43B3CB1B8 CRC64;
                                                                                                                                                                             POTENTIAL.
RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                           46.5%; Score 270.5; DB 1.
43.6%; Pred. No. 2.4e-23;
tive 19; Mismatches 36
                                                                                                                        PROSITE, PS00127; RNASE_PANCREATIC, 1. Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                             1 21 P
22 132 R
132 AA; 14625 MW;
                                                                      Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
                       InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                     ilarity 43.6%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae, Xenopus.
NCBI_TaxID=8355;
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nes 39; Conserv
                                                                                                                                                                                                                                                                                                     Similarity
48; Conserv
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HSSP; P11916; 1BC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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Q98SL8
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Matches
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         RT DDR DDR ET SO DR E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 WLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKNVL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 WAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSNVL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catesbeina (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Raniae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catebbelana (Bull frog).
60 TISEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 SPTRPQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%; Score 281; DB 13; Length 132; 47.7%; Pred. No. 1.5e-24; ative 14; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                             132 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00074; InaseA; 1.
ProDom, PD000535; RNaseA; 1.
SMART; SM0092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RC-RNASE7
                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Created)
                                                                                                                                                                                          PRT;
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23 132 RG
132 AA; 14412 MW;
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                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
                                                                                                                                                                                                                    Q98SM2;
01-JUN-2001
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                                                                                                                                                                                          Q98SM2
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Matches
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                                                                                                                                                     Q98SM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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MEDILINE-2139506, PubMed=11683320,
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENOYPVHFAGIGOC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 LITSEFYLSDCN---VISRPCKYKLKKSINIFCVICENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                  th 48.3%; Score 281; DB 13; Length 1. Similarity 47.3%; Pred. No. 1.5e-24; 52; Conservative 17; Mismatches 33; Indels
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                                                                                                 GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                    1 22 POTENTIAL.
133 AA; 14615 MW; C8785B236B26E54E CRC64;
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BB40B9A94FA5B943 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rana catesbelana (Bull frog).
Eukaryota; Metacza; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 47.6%; Score 277; DB 13; Similarity 46.4%; Pred. No. 4.3e-24; 51; Conservative 18; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1.
Probom, PD000535; RnaseA; 1.
SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                 Probom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL 1 22 PC
SEQUENCE 133 AA; 14590 MW;
bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF351210; AAK30256.1; -.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Evol. 53:31-38(2001)
EMBL; AF351211; AAK30257.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001427; RNaseA.
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Q9DFY7

RESULT 5

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09DFY7

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3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSRD 84
                                                                                   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIATRE=2139506; PubMed=11683320;
ROSEnberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                    GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
                                                                                                                                                                                                                                                                                                                                   RC-RNASE6 RIBONUCLEASE.
AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87FCF122C3499E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       Score 304; DB 13;
Pred. No. 3.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.3%; Score 293; DB 13; 49.1%; Pred. No. 6.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNase A-type ribonuclease rc208 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
ProDon; PD000535; RNaseA; 1.
SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                 Pfam; PF00074; rnaseA; 1.
ProDcm; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
    Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA; 14628 MW;
                                                                                                                                                                                                                                                                                                                                                             14804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bullfrog, Rana catesbeiana."
J. Mol. Evol. 53:31-38(2001)
EMBL; AF351209; AAK30255.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001427; RNaseA.
                                                                                                                          EMBL; AF242556; AAG31442.2;
HSSP; P22069; 10NC.
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                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                        24 1
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                           SEQUENCE FROM N.A.
                                                                 rissum=Liver;
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                                                                                                                                                                                                                                                                                                  Signal
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25 DWETFOKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSRD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordařa; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DFY5 PRELIMINARY; PRT; 128 AA.
O9DFY5 D3DFY5
01-MAR-2001 (TEMBLrel. 16, Created)
01-OCT-2001 (TEMBLrel. 18, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Rana catesbeiana (Bull frog).
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
MCBI_TAXID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20512555; PubMed=11058105; Laio Y.D., Buang B.C., Wang S.C.; Lao Y.J., Buang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog)."; Mucleic Acids Res. 28:4097-4104(2000). EMBL; AF242554; AAG31440.2; Lissp: P22069; 10NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Liver;
MEDLINE-20512555; PubMed-11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%; Score 306; DB 13; Length 128; Best Local Similarity 54.4%; Pred. No. 1.9e-27; Matches 56; Conservative 12; Mismatches 35; Indels (
                                                               EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                     BFYLSDCMRIKLPCHYKLKKSSNTICITCENKLPVHFVAVBEC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 EFYLSDCNVTSRPCKYKLKKSTNTPCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 AFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                             128 AA.
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                             RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14517 MW;
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                                                                                                                                                                                                             PRELIMINARY;
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128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Liver;
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Signal. SIGNAL

RESULT 6 O9DFY5

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62

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25 DWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGFVKALCRGVIFSADVLSNS 84
                                                                  Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, RF242555, AAG31441.2;
PDB; 1KVZ; 28-UUL-02.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Ranoidea; Ranoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.6%; Score 399.5; DB 13; Length 129; 67.3%; Pred. No. 3.1e-38; tive 16; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., valumited (AdG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242553, AAG31439.1; -.
PDB; 1M58; 09-JAN-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 EFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          24 129 RC-RNASE4 RIBONUCLEASE.
129 AA; 14724 MW; 826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
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67.0%; Pred. No. 4.2e-36;
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                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 PO
128 RC
14839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 67.3
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Conservative
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129
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128 AA;
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Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bulifrog).";
Nucleic Acids Res. 28:4097-4104(2000).
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                                                                                                                      SEQUENCE FROM N.A.
Liao Y.-D., Wang S.-C.;
Liao Y.-D., Wang S.-C.;
Liao Piplens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332139; AAL54383.1;
PIR, A99035; R39035.
GO; 00004522; F:nucleic acid binding; IEA.
GO; GO:0004522; F:nucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
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127 AA; 14469 MW; 953F90D35ICFEEF3 CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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Rana catesbeiana (Bull frog).
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                        3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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1 MSDWLJFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105
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3.5	Description	Q9i8v8 rana pipien	rana	Q9dfy6 rana catesb	Q9dfy8 rana catesb	Q9dfy7 rana catesb	Q9dfy5 rana catesb	Q98sm0 rana catesb	Q98sm2 rana catesb	Q98s19 rana catesb	Q98s18 rana catesb	Q98sm1 rana catesb	Q9df78 rana catesb	Q9w738 xenopus lae	Q9jki5 mus saxicol	Q9jki9 meriones un	09/ki7 mus saxicol
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                                                                                                                                                                                                                                                                                                                             Mus saxicola (Spiny mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20243759; PubMed=10758160; Zhang J., Dyer K.D., Rosenberg H.F.; Zhang J., Dyer K.D., Rosenberg H.F.; Zhang J., Dyer K.D., Rosenberg H.F.; Evolution of the rodent eosimophil-associated ribonuclease gene family by rapid gene sorting and positive selection."; Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000). HSSP; P10153; 11172. GO; GO:0003676; F:nucleic acid binding; IEA. GO; GO:0004522; F:pancreatic ribonuclease activity; IEA. InterPro; IPRO01427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 152 AA; 16830 MW; 780421C3661732C8 CRC64;
                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
Eosinophil-associated ribonuclease 10.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Eosinophil-associated ribonuclease 44.
                                                            152 AA
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                                                   PRELIMINARY;
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Les 37; Conserv
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SEQUENCE FROM N.A.
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ID Q9JKIS
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                          Length 157;
                                                                                                                                                                                                                   37; Indels
                                                                                                                                                                                                                                                       1 SDWLTFOKKHLTNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPV-
             Pfam, PP00074; rnasea, 1.
PRINTS; PR00794; RIBONUCLEASE.
Prodom, PD000538, RNasea, 1.
SWART; SM00022; RNASe Pc; 1.
PROSITE; PS00127; RNASE Pancreatic; 1.
SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;
                                                                                                                                                                   22.7%; Score 131; DB 11; 30.6%; Pred. No. 3.2e-07; iive 20; Mismatches 37;
InterPro; IPR001427; RNaseA.
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Best Local Similarity 30.6:
Matches 34; Conservative
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FRL2 protein.
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288642; AAG30414.2;
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
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                                                                                                                                                                                                                                                                                                                 MEDLINE-21539506; PubMed=11683320; Rosenberg H. P., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H. P., Zhang J., Liao Y.-D., Dyer K.D.; Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana."; J. Mol. Evol. 53:31-38(2001). BMBL; AF351208; ARX30254.1; -- HSSP; P11916; LBC4. GO; GO:0004525; F:pancreic acid binding; IEA. GO; GO:000422; F:pancreadic ribonuclease activity; IEA. InterPro; IPR001427; RNaseA.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
RO-CCT-2003 (TrEMBLrel. 25, Last annotation update)
RO-CRABSeLI ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                               Rana cateŝbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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MEDLINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 275; DB 13; Length 132;
48.2%; Pred. No. 6e-24;
tive 14; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 22 POTENTIAL.
132 AA; 14704 MW; 95D61760F729868E CRC64;
                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                            132 AA.
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                                                                                                                                                       RNase A-type ribonuclease rc204 precursor.
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ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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Nucleic Acids Res. 28:4097-4104(2000)
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                                            PRT;
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Conservative 1
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Matches 53; Conserv
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                                            Q98SM1
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  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 FMEKHIVKEGAETNCNOTIKDRNIRFKN--NCKFRNIFIHDINGKKVKEMCAGIVKSTFV
                                                                                                                                                                                                                                                                                                                                                                                          2 DWLTFQXXHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVXAICKGIIASKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a seast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
NCBI_TaxID=8355,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCYTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169;
                                                                                                                                                                                                                                                                                         DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 LITSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                       46.9%; Score 270.5; DB 13; Length 43.6%; Pred. No. 2e-23; tive 19; Mismatches 36; Indels
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
PFam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS9166; AAD41901.1;
HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:panoreatic ribonuclease activity; IEA
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                 POTENTIAL.
RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 157.5; DB 36.1%; Pred. No. 3e-10; ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AA
                                                                                                      SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96069863; Pubmed=7585965;
                                                                                                                                                                                   1 21 P
22 132 R
132 AA; 14625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 36.18 nes 39; Conservative
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Kosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
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MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rna catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordača, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 TISBFYLSDC---NVISRPCKYKLKKSINTFCVICENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTRFQLDTCTRISITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.7%; Score 281; DB 13; Length 132; 47.7%; Pred. No. 1.2e-24; tive 14; Mismatches 35; Indels {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF551207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11916; 1864.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RC-RNASE7.
; 131A745187978687 CRC64;
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01-OCT-2003 (TEMBLrel. 25, Last annotation update)
                                                                       132 AA
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Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 AA; 14412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
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                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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les 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                             Q98SM2;
                                                              Q98SM2
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Matches
RESULT 8
2988M2
AC 0988S
AC 0988S
DT 01-0
DT 01-0
DT 01-0
DE RABA
OC ENAB
OC ENAB
OC AMBPH
OC
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                                                                                                                                                                                                                                                                                                2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPBPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                   24 NWATFQQKHITNTSSINCSNIMNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKKV
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21539506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; "Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana :a1esbeiana."; J. Mol. Evol. 53:31-38(2001). EMBL; AF351211; AAK30257.1; -... HSSP; P11916; 1864.
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.7%; Score 281; DB 13; Length 133; ilarity 47.3%; Pred. No. 1.2e-24; Conservative 17; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%; Score 277; DB 13; Length 1:
46.4%; Pred. No. 3.6e-24;
1°. Mismatches 33; Indels
                                                          GO, GO:00036'6; F.nucleic acid binding; IEA.
GO, GO:0004522; F.pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA.
Probom; PF0000535; RNaseA.
PROSITE; SM00092; RNASE_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                       1 22 POTENTIAL.
133 AA; 14615 MW; C8785B236B26E54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                J. Mol. Evol. 53:31-38(2001).
EMBL; AF351210; AAK30256.1; -.
HSSP; P11916; 1BC4.
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SEQUENCE 133 AA; 14590 MW;
   Rana catesbeiana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                    52;
bullfrog,
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                          Signal.
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Q98SL8
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Nucleic Acids Res. 28:4097-4104(2000).
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128 AA;
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Matches 54; Conserv
                        SECUTENCE FROM N.A.
                                                                                                                                                                                                 SEQUENCE
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Best Local
                                                                                                                                                                 Signal.
                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                        CHAIN
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Q98SM0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 DWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSRD 84
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE=20512555; PubMed=11058105;
MEDLINE=20512555; PubMed=11058105;
MEDLINE=20512555; PubMed=11058105;
Medicariow, Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDIJINE=20512555; PubMed=11058105;
MEDIJINE=20512555; PubMed=11058105;
Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 306; DB 13; Length 128; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 1294.097-4104 (2000).

EMBL, AF242554; AAG31440.2; -.

HSSP, P22069; 10MC.

GO; GO:0004522; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonucleasp activity; IEA.

InterPro; IPR001427; RuaseA.

Priam; P500074; rnaseA; 1.

Probom; P2000535; RNaseA.

PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                     EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                  RC-RNASE3 RIBONUCLEASE.
2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Last a
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                             RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 23 PC
24 128 RC
128 AA; 14517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
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Best Local S
                25
                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.
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                                                                                                                                    09DFY7;
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                                                                                                                      Q9DFY7
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                                                                                               RESULT 5
Q9DFY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 DWDTFQKKHLTDTKKVKCDVEMKKALFDCKKINTFIFARPFRVQALCKNIKDNTNVLSRD 84
TISSUE-Liver;
Liaco Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AAG31442.2; -.
HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFLYSRPEPVKALCKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 DWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelan.";
J. Mol. Evol. 53:31-38(2001).
EMBL, ARS12509; AAK30255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TERMBLE-1 17, Last sequence update)
01-OCT-2003 (TERMBLE-1 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana. NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LITSEFYLSDC---NVTSRPCKYKLKKSINIFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 VFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P11916; 1864.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                    GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 POTENTIAL.
14628 MW; 87FCF122C3499E02 CRC64;
                                                                                                                                                                                                                                                                                                                                   RC-RNASE6 RIBONUCLEASE. SPEBFD67D266C7C2 CRC64;
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49.1%; Pred. No. 5e-26;
iive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 304; DB 13;
Pred. No. 2.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AA
                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                     Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                 14804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  52.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity 53.43
55; Conservative
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2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPBPVKAICKGIIASKNVLTTS 61
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24 1
128 AA;
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Best Local Similarity
                        SEQUENCE FROM N.A.
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                                                    TISSUE-Liver;
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SIGNAL
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Q9DFY8;
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SIGNAL
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61
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01-OCT-2001 (TYEMBLrel. 18, Last sequence update)
01-OCT-2003 (TYEMBLrel. 18, Last sequence update)
RC-RNase4 ribonuclease precursor.
RC-RNase4 ribonuclease precursor.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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Liac Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog)...,
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                                                                                         EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Lido Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332139; AALS4383.1; -.
EMBL; AF332139; AALS4383.1; -.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Northern leopard frog).
                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onconase precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana pipiens
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1D Q8UV
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, $7242555, AAG31441.2; -.

EMBL, $7242555, AAG31441.2; -.

EDB, 1KVZ, 28-JUL-02.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:000422; F:pancreatic ribonuclease activity; IEA.

Interpro; IPR001427; RNaseA.

ProDon; PD000535; RNaseA; 1.

PROSITE; PS00127; RNASE_PANCREATIC; 1.
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BMBL, AF242523, AAG31439.1; -. BMBL, BMBL, BMBB, BMB, BMBB, BMBB, BMB, BMBB, BMBB, BMB, BMB
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Nucleic Acids Res. 28:4097-4104(2000).
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24 129 RC-RNASE4 RIBONUCLEASE.
129 AA; 14724 MW; 826A62882B10ABDA CRC64;
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
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7, 2004, 21:29:10 ; Search time 29.5753 Seconds (without alignments) 1109.503 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

rvirus:* bacteriap:*

sp_archeap:*

SUMMARIES

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Q9i8v8 rana pipien Q8uvx5 rana pipien Q9w738 xenopus lae mus saxicol rana rana rana rana rana rana rana rana rana Description QBuvx5 Q9dfy6 Q9dfy8 Q9dfy7 Q9dfy5 Q98sm0 Q98sm2 Q98sm2 Q98sm3 Q98sm3 Q98sm3 O9jkis O9jki9 O9jki7 Q98SL8 Q98SM1 298SM2 **538819** 29DF78 Q9W738 29DFY5 **0MS86C Q918V8** 29DFY6 29DFY7 DB Query Match Length 99.3 275 270.5 157.5 133 131 130.5 Score 551 399.5 304 293 281 381 281 Result

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ALIGNMENTS

RESULT 1

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"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure.";
Nucleic Acids Res. 28:2375-2382(2000).
BIRL, AF165133; AAF76935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0nconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frogl).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibja; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBL_TaxID=8404;
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Pred. No. 2e-58;
0; Mismatches 0; Indels (
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:nucleatic ribonuclease activity; IEA.
InterPro; IPR00427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Probom, PD000535; RNaseA; 1.
SMART; SM00922; RNASE Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
B8511DC5407AB69B CRC64;
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100.0%; Pred. No. 2.
... 0; Mismatches
            127 AA
            PRT;
                                                                                                                                                                                                 MEDLINE=20330357; PubMed=10871370;
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Best Local Similarity 100.0
Matches 103; Conservative
             PRELIMINARY;
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SEQUENCE FROM N.A.
TISSUE=Liver;
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               Q918V8
918V8
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2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS

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mus saxicol

Q9JKIS Q9JKI9 Q9JKI7

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Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=2024759; PubMed=10758160;

Zhang J., Dyer K.D., Rosenberg H.F.;

"EVOLUTION of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection.";

Proc. Matl. Acad. Sci. U.S.A. 97:4701-4706(2000).

EMBL; AF238394; AAF67694.1; -.
                                                                                                                                                                                                                                                                                                                Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom. PD000535; RNaseA; 1.
SWART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
SEQUENCE 157 AA; 17945 MW; FDFE22FE77FE371A CRC64;
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GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

InterPro; IPR001427; RNaseA.
                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                           Fosinophil-associated ribonuclease 25
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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PRINTS; PR00794; RIBONUCLEASE.
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Best Local Similarity 29.28
Matches 33; Conservative
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                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=10047;
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29JKI9
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Search completed: May 7, 2004, 21:46:02 Job time : 30.8597 secs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFlYSRPEPVKAICKGIIASKNVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Gaps
                                                                                                                                                         Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-20243759; PubMed=10758160; Zhang J., Dyer K.D., Rosenberg H.F.; Zhang J., Dyer K.D., Rosenberg H.F.; Evolution of the rodent eosinophil-associated ribonuclease gene family by rapid gene sorting and positive selection."; Perc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000). HSSP; P10153; HILZ. GO: 60:0003676; Finucleic acid binding; IEA. GO: Go:0004522; Fipancreatic ribonuclease activity; IEA. Interpro; IPR01427; RNsseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ȚFE-----FYLSDCNATS----RPCKYKLKKSTNTFCVTCENQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.5%; Score 120; DB 11; Length 157; 29.2%; Pred. No. 5.4e-06; ative 18; Mismatches 34; Indels 28
         157 AA
       PRT;
  PRELIMINARY;
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---KAICKGII 53
                                                                                                                                                                                          Gaps
                                                                                                                                         20;
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                                                                                                     Length 157;
                                                                                                                                                                                                                                             54 ASKNVL-TTFEFYLSDCNATS-----RPCKYKLKKSTNTFCVTCENQAP
                                                                                                                                       Indels
                                                                                                                                                                    4 WLIFQKKHLINIRDVDCN-NILSINLF--HCKDKNTFIYSRPEPV-
Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;
                                                                                            20.5%; Score 120; DB 11; J
29.4%; Pred. No. 5.4e-06;
Live 20; Mismatches 37;
                                                                                                                                 32; Conservative
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FRL2 protein.
FRL2.
                                                                                                           SEQUENCE
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SIGNAL
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                                                                                                CHAIN
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EMBL; AF288642; AAG30414.2; --
HSSP, P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 QDWLIFQKKHLINIRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKALCTGVLNS-N
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranodae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDIJINE=20512555; PubMed=11058105;
MEDIJINE=20512555; PubMed=11058105;
Jiao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
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8
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47.7%; Pred. No. 1.7e-23;
tive 13; Mismatches 37; Indels
                                                                                                                                                                                                                 bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38 (2001).

EMBL; AF351208; AAK30254.1; -1.

HSSP; P11916; 1BC4.

GO; GO:0003876; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

InterPro; IFPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                              132 AA; 14704 MW; 95D61760F729868E CRC64;
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                              132 AA
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ProDom; PD000535; RNsseA; 1.
SMART; SMO092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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Best Local Similarity
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22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Best Local Similarity 36.1%; Pred. No. 5.7e-10;
Matches 39; Conservative 18; Mismatches 36; Indels 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
45.5%; Score 265.5; DB 13; Length
Best Local Similarity 43.2%; Pred. No. 5.6e-23;
Matches 48; Conservative 18; Mismatches 38; Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF159166; AAD41901.1; --
HSSP; P00656; ILSQ.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
PFam; PF00074; rnaseA; 1.
GO, GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
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D8D9A517452FBE53 CRC64;
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Last annotation update)
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SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                    1 21 P
22 132 R
132 AA; 14625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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9

82 VLSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132

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23 QTWAKRQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ODWLTFOKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                     MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNase A-type ribonuclease rc212 precursor.
Stana catesbeiana (Bull frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae, Rana.
                                                                                                                                                 Euteleostomi;
Ranidae; Rana
                                                                           01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rna catesbeiana (Bull frog).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi.
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Indels
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF35578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 132 RC-RNASE7.
132 AA; 14412 MW; 131A745187978687 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.8%; Score 279; DB 13; 47.7%; Pred. No. 1.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17. Last sem
                                                                                                                                                                                                                                                                                       bullfrog, Rana catesbeiana.";
                                                                                                                                                                                                                                                                                                       Mol. Evol. 53:31-38(2001).
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                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                 NCBI_TaxID=8400;
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01-JUN-2001
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                                                Q98SM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                              098SM2
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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MEDINE=21539506; PubMed=11683320;
MEDINE=21539506; Dubmed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.",
J. Mol. Evol. 53:31-38(2001).

EMBL; AF351211; AAK30257.1; -.
HSSP; P1916, 1BG4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordaľa; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 VLSSTKRQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 VLTTFEFYLSDCN---ATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 VLTTFEFYLSDCN---ATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Indels
                                                                                                               GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA. 1.
SMART; SM00092; RNAse_Pc; 1.
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SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 276; DB 13;
46.8%; Pred. No. 3.4e-24;
tive 16; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFGM, PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                    PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
bullfrog, Rana catesbeiana.";
J. MOJ. Evol. Evol.
EMBL, AFS51210; AAK30256.1;
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                1 22 Po
133 AA; 14615 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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098SL8
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Q9DFY7

RESULT 5 Q9DFY7

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2 QDWLTFQKKGLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGILASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AFA42556; AAG31442.2;
HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-21533506; PubMed=11683320;
ROSenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the "rapid stars catesbeara".";
J. Mol. Evol. 53:31-38(2001).

EMB. APS12109; AAX30255.1;

HSSP; Pil916; 1BA4.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNase A-type ribonuclease rc208 precursor.
Stana catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ULTTFEFYLSDCNATS---RPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 50.0%; Score 292; DB 13; Length 133; Local Similarity 49.5%; Pred. No. 4.7e-26; hes 55; Conservative 14; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                            HSSP; P22069; IONC.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                    23 POTENTIAL.
128 RC-RNASE6 RIBONUCLEASE.
14804 MW; AFEBFD67D266C7C2 CRC64;
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B7FCF122C3499E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0UN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            / Match 52.2%; Score 305; DB 13; Local Similarity 52.9%; Pred. No. 1.4e-27; Les 55; Conservative 14; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AA
                                                                                                                                                                                                                     Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
            Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
14628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      24 1
128 AA;
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                                              SEQUENCE FROM N.A.
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                                                                  IISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q98SM0;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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SIGNAL
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Q98SM0
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2 QDWLTFQKKGLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-2051255; PubMed=11058105;
A Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
The Publification and cloning of cytotoxic ribonucleases from Rana catesbeinan (bullfrog).";
Nucleic Acids Res. 28:4097-4104 (2000).
R EMBL, AF242554; AAG31440.2;
R EMBL, AF242554; AAG31440.2;
R ESP; P22069; IONC.
R EMBL, AF24225; Francleic acid binding; IEA.
R GO; GO:0003676; Francleic acid binding; IEA.
R GO; GO:0004222; Francreatic ribonuclease activity; IEA.
R InterPro; IPRO1427; RNASSA.
R PRODOM; PD000535; RNASSA; I.
R PROSITE; PS00127; RNASB_PANCREATIC; I.
                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasca ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
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                                                                              62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
RC-RNASE3 RIBONUCLEASE.
; 2B14986082E0587D CRC64;
                                                      62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 307; DB 13;
; Pred. No. 8.2e-28;
13; Mismatches 35;
                                                                                                                                                                                                 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Last RC-RNase ribonuclease precursor. Rana catesbeiana (Bull frog).
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14517 MW;
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                                                                                                                                                                                             PRELIMINARY;
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128 AA;
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
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SIGNAL
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CHAIN

Matches

Q9DFYS ID Q9DFYS

RESULT 6

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Wang S.-C.;

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2 QDWLIFQKKHLINIRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLIT
                    TISSUE=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., <sup>1</sup>
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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128 AA;
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129 AA;
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les 69; Conserv
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  SEQUENCE FROM N.A.
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Best Local
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SIGNAL
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2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbaiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                         SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lido Y. D., Mang S. -C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF32139; AAL54383.1;
PIR; A39035; R39035.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
PIRAFPIC: IRRO01427; RNASEA.
PFO0074; INASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  953F90D351CFEEF3 CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 93.0%; Score 543; DB 13; Score 543; DB 13; Similarity 93.3%; Pred. No. 3.1e-55; 97; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                    127 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNAŠE_PANCKEATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern leopard frog)
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                                                                                                                                                                                                                                                                                                                               Onconase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=8404;
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF24253; AAG31439.1; --
PDB; IMSB; 09-CAM-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
PFGam; PF000074; rnaseA.
Probom; PD000535; RNaseA, 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 QDWATFKKKHLIDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGFVKALCRGVIFSADVLSN
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Rana catesbeiana (Bull frog).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                     DB 13; Length 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 FEFYLSDCNATSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                  67.0%; Score 391.5; DB 13; Length
64.8%; Pred. No. 1.3e-37;
iive 17; Mismatches 19; Indels
EMBL; AF242555, AAG31441.2; -...
PDB; IKVZ; 28-JUL-02.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004222; F:pancreatic ribonuclease activity; IEA.
Interpro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                  826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                 POTENTIAL.
RC-RNASE4 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                              Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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14839 MW;
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14724 MW;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:29:10 ; Search time 29.8597 Seconds Run on:

(without alignments) 1109.503 Million cell updates/sec

US-09-961-400-8

584
1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Perfect score: Sequence:

BLOSUM62 Scoring table:

1017041 segs, 315518202 residues Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

SPTREMBL_25:*

: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
5: sp_tungi:*
5: sp_tunvertebrate:*
5: sp_mammal:*
5: sp_mhc:*
5: sp_organelle:*
5: sp_organelle:*
5: sp_organelle:*
5: sp_organelle:*
5: sp_organelle:*
5: sp_organelle:*

sp_unclassified:* sp_vertebrate:* sp plant:*
sp rodent:*
sp_virus:* 10: 112: 123: 14: 16: 17: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp_archeap:*

Description			ב מבונט	י מוומ	t dild	י מווט	Courtys fand catesb	ralla	Uyesmz rana catesb	Q98sl9 rana catesb	098sl8 rana catesh	בחבת	rana		Contrac ventobus rue	Talkla meriones un	O9jki9 meriones un	Q861y3 pygathrix r
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SUMMARIES ID	O9TRVA	OBUVX5	OSDEY6	O9DFY8	O9DFY7	O9DFY5	OWS WO	00000	25000	CARSTO	Q98SL8	098SM1	Q9DF78	09W738	OQ.TK.T2		CAUKIB	Q861Y3
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Score	565	543	391.5	382	307	305	292	279	320	0 / 7	7/7	270	265.5	154.5	120	100	071	119.5
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146 6 Q861Y2 146 6 Q861Y1 157 11 Q9JKJ4	1111	111		147 6 Q8HZQ0 119 6 Q9TV30 154 11 Q9JKI8	11 6 11 6	9119	144 11 Q80285 153 11 Q90XS4 155 11 Q9JKI6 119 6 Q9TV31 155 11 Q9JKI2
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1112 0967	222	4.00	7 8 8 7	32	33 34 36 36	37 38 39	4 4 4 4 4 1 4 4 4 4 6 1 6 4 6

Chen S.-L., Le S.-Y., Newron D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual langth and structure.";
Nucleic Acids Res. 128.2375-2382(2000).
EMBL; AF165133; AAF76935.1;
P.TR, A39035; A39035.
HSSP; P22069; IONC.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA. 01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last amotation update)
01-OCT-2003 (TrEMBLrel. 25, Last amotation update)
00-COMPAGE variant raphul precursor.
Rana pipiens (Northern leopard frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana. 96.7%; Score 565; DB 13; Length 127; 97.1%; Pred. No. 8.7e-58; ive 1; Mismatches 2; Indels 1 23 POTENTIAL. 127 AA; 14491 MW; B8511DC5407AB69B CRC64; 127 AA. PFam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SWART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1. PRT; SEQUENCE FROM N.A. TISSUE-Liver; MEDLINE=20330357; PubMed=10871370; PRELIMINARY; Matches 101; Conservative Local Similarity SIGNAL Query Match **0918V8** RESULT 1 **0918V8**

2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pygatňrix roxellana (golden snub-nosed monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
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SEQUENCE FROM N.A.
Zhang J., Zhang Y.-P.;
"Fseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                 MEDLINE=22597544; PubMed=12711394;
Zhang J., Zhang Y.-P.;
"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 22.2%; Score 129.5; DB 6; Length 146; Local Similarity 34.2%; Pred. No. 4.2e-07; les 38; Conservative 16; Mismatches 40; Indels 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vene JUB:20-101/2003).
BMBL, AY221130, AA041337.1; -.
GO, GO:00004576; F:nucleic acid binding; IEA.
GO, GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro, IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00074; rnaseA; 1.

PRINTS; PR00794; RIBONUCLEASE.

ProDom; PD000535; RNASeA; 1.

SMART; SM0092; RNASe Pc; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                               Last sequence update)
Last annotation update)
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                    146 AA
                                                   Created)
                    PRT;
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                                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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                    PRELIMINARY;
                                                                                                                                                                                                                                                                 eating monkey.";
Gene 308:95-101(2003)
                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                          Pygathrix.
NCBI_TaxID=61622;
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Q861Y3
ID Q861Y3
DT Q1-JUN-2003 ('
DT 01-JUN-2003 ('
DE ANGIOGENIN.
OS PYGACHTIX TOX
OC ENKARYOCT; MC
OC MAMMALIA; EUL
OC PYGACHTIX.
OC PYGACHTIX.
OC NOBLITAXIDE61
RN [1]
RN HEDLINE=2597
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OCH TAXIDE61
RY MEDLINE=2597
RA CANDONEY
RY MEDLINE=2597
RA CANDONEY
RY MEDLINE=2597
RA CANDONEY
RY GENE 308:95-11
DR GO; GO:000367
DR GO; GO:000367
DR PFGM, PROOFF
DR PRINTS; PROOFF
DR PROSTITE; PSOG
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Matches
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RESULT 11

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2 QDWLIFQKKHLINIRDVDCNNIMSTNLF----HCKDKNIFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                   22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 FWEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                           58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                      82 ELSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132
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                                                                                                                                                                                                                               DB 13; Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 LITSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0004522; F:pancreatic ribonuclease activity; IEA. InterPro; IPR001427; RNaseA. Ffam; PF00074; rnaseA; 1. Propor; PR00074; RNaseA; 1. SMO00935; RNaseA Pc; 1. SMART; SM00092; RNASE_Pc; 1. PROSITE; PS00127; RNASE_PanCREATIC; 1.
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kinoshita N., Kirschner M.W.;
Kinoshita N., Kirschner M.W.;
Submitted (JUW.) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1551466; AAD41901.1;
HSSP; P00556; ILSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.
InterPro; IFR01427; RNaseA.
Pfam; PF00074; rnaseA: 1.
                                                                                                                                              1 21 POTENTIAL.
22 132 RC-RNASEL1 RIBONUCLEASE.
132 AA; 14625 MW; D8D9AS17452FBE53 CRC64;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 1889] MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                          47.3%; Score 275.5; DB 13;
44.1%; Pred. No. 4 6e-24;
witnest 36;
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Best Local Similarity
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                                                                                                                                                                                                                                                                      49;
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF28642; AAG30414.2; -.
HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfroy, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; APS51208; AAX30254.1;
HSSP; P11916; 1BC4.
                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease roc204 precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordaľa, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 VLITSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENBYPVHFAGIGKC 132
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Nucleic Acids Res. 28:4097-4104(2000).
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
95D61760F729868E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TIEMBLrel. 16, Created)
01-0CT-2001 (TIEMBLrel. 18, Last sequence update)
01-0CT-2003 (TIEMBLrel. 12, Last annotation update)
RC-RNAsell ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 280; DB 13; 48.6%; Pred. No. 1.4e-24;
                                        132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000535; RNaseA; 1.
SWART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AA; 14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batraci
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                    Q98SM1;
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RESULT 12

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9

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RESULT 14

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1 22 P
23 132 R
132 AA; 14412 MW;
      EMBL; AF351207; AAK30253.1; -. EMBL; AF359578; AAL87036.1; -. HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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Q98SL8
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         SO THE PROPERTY OF THE PROPERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 QNWATFQQKHITNTSSINCSNIMMNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21539506; PubMed=11683320;
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeinan";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF351210; AAK30256.1; -.
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MEDILINE-21239506; PubMed=11683320;
KSOSENDE-11 H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBL_TaxID=8400;
58 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-07N-2001 (TrEMBLrel. 17, Created)
01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNASe A-type ribonuclasse rc203 precursor (RC-RNase7 precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.1%; Score 286; DB 13; 47.7%; Pred. No. 2.8e-25;
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                                                                                                                                                                                             133 AA
                                                                                                                                                                                                                                                                                                                                                 RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 P(
14615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana catesbeiana."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.78;
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                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           Q98SL9;
                                                                                                                                                                                             Q98SL9
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Q98SM2
                                                                                                                               RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ODWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81
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MEDLINE-2159506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. MOI. EVOI. 53:13181201);
BAR302571;
HSSP; P11916; 1BC4.
GO; GO:0004522; F:nucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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46.8%; Pred. No. 8.2e-25;
iive 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                             Length 132;
                                                                                                                                                                                                                                                                                                                                                                         48.9%; Score 285; DB 13; Length 1
47.7%; Pred. No. 3.7e-25;
tive 14; Mismatches 36; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00922; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                  131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNase A-type ribonuclease rc218 precursor. Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                  POTENTIAL.
RC-RNASE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98SL8;
01-JUN-2001 (TrEMBLrel. 17, Created)
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Q9DFY7

RESULT 5 Q9DFY7

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2 QDWLTFQKKGLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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                                                                                                                              Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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SEQUENCE FROM N.A.

MEDLINE=21539506; PubMed=11683320;

ROSemberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana ";
J. Mol. Evol. 53:31-38(2001).

BENBL; AF351209; AAK30255.1; -.

HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Rana catesbejana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                          GO, GO:0005676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Plam; PF00074; rnaseA,
Probom; PD000535; RNaseA, 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; 30:0003676; F:nucleic acid binding; IEA.
GO; 30:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 RC-RNASEG RIBONUCLEASE.
14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87FCF122C3499E02 CRC64;
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51.1%; Score 298; DB 13; I
Best Local Similarity 49.5%; Pred. No. 1.2e-26;
Matches 55; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.0%; Score 309; DB 13; Best Local Similarity 53.8%; Pred. No. 5.9e-28; Matches 56; Conservative 13; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
               Nucleic Acids Res. 28:4097-4104(2000).
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                      EMBL; AF242556; AAG31442.2; -. HSSP; P22069; 10NC.
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14628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 1
128 AA;
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SEQUENCE 133 AA;
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8400;
                                                                                                  ISSUE=Liver;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
SIGNAL
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Q98SM0
               REPRESENT OF THE PRICE OF THE P
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                                           83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR 83
24 ONWEIFORKHLIDIRDVKCDAEMKKALFDCKQKOTFIYARPGRVQALCKNIIVSKNVLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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RC-RNase6 ribonuclease precursor.
Rana catebolana (Bull frog).
Bukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512555; PubMed=11058105; Jang P.C., Wang S.C.; Jaco Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; Putification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog)...,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Buang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                           84 DEFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127
                                                                                            62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 DAFLLPQCDRIKLPCHYKLSSSTWIICITCWNOLPIHFAGVGSC 127
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00774; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
RC-RNASE3 RIBONUCLEASE.
; 2814986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2001 (TrEMBLrel. 18, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) RC-RNase3 ribonuclease precursor.
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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54.8%; Pred. No. 3.5e-28;
tive 12; Mismatches 35;
                                                                                                                                                                                                                                                                                                        128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 28:4097-4104(2000)
EMBL; AF242554; AAG31440.2; -.
                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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24
128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8400;
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01-OCT-2001
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Signal.

Matches

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HSSP;

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Q9DFY5

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Length 129;

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RESULT 2

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2 QDWLFFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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EMBL, AF242523, AAG31439.1; -.
EDB; 1M58; 09-JNN-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:000452; F:panoreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
ProDom; PD000535; RNaseA; 1.
                <code>TISSUE=Liver;</code> Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., Purificacin and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog) ", Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%; Score 386; DB 13; Length 128; 67.3%; Pred. No. 7.1e-37; tive 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                     ;; Score 404.5; DB 13; Length
;; Pred. No. 5.1e-39;
16; Mismatches 17; Indels
                                                             EMBL; AF242555; AAG31441.2; -
PDB; 1KVZ; 28-JUL-02.
GO; GO:0003676; F:nucleatic acid binding; IEA.
GO; GO:0004222; F:pancreatic ribonuclease activity; IEA.
INTERPRO; IPR001427; RNaseA.
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989719CF52053ECC CRC64;
                                                                                                                                                                                                                                                      826A62882B10ABDA CRC64;
                                                                                                                                                                                                                     POTENTIAL.
RC-RNASE4 RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                     23 PC
129 RC
14724 MW;
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14839 MW;
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Best Local Similarity 6.....
And 71; Conservative
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128 AA;
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129 AA;
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nes 70; Conserva
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                         SEQUENCE
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                  83
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Gaps
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Rama catesbelana (Bull frog).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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Pred. No. 1.4e-56;
2; Mismatches 2; Indels
                                                    SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                      SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                 PIR; A39035; A39035.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                        01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                          127 AA
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SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                               Rana pipiens (Northern leopard frog)
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nes 100; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Onconase precursor.
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Best Local
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

7, 2004, 21:29:10 ; Search time 29.8597 Seconds (without alignments) 1109.503 Million cell updates/sec Мау

US-09-961-400-6 583 1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_25:*
1: Sp archea:*
2: sp_bacteria:*
3: sp fungi:*
4: Sp human:*
5: sp_invertebrate:*
5: Sp mammal:*
5: Sp mammal:*
5: Sp organelle:*
8p organel:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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•	* Query	Match	99.1	95.4	69.4	66.2	53.3	53.0	51.1	49.1	48.9	48.4	4.8	7.0	7.1	27.0	22.2	22.3	1	22.2
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152	157	153	157	146	157	154	157	147	157	155	155	147	155	132	155	155	146	132	170	119	119	147	155	156	156	119	155	155
22.1	21,8	21.7	21.6	21.5	21.4	21.1	20.9	20.8	20.8	20.7	20.5	20.2	20.0	19.8	19.8	19.8	19.7	19.6	19.6	19.5	19.5	19.5	19.5	19.4	19.4	19.3	19.3	19.3
129	127	126.5	126	125.5	125	123	122	121	121	120.5	119.5	118	116.5	115.5	115.5	115.5	115	114.5	114.5	113.5	113.5	113.5	113.5	113	113	112.5	112.5	112.5
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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us-09-961-400-4.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 TFE-----FYLSDCNVTS-----RPCKYKLKKSTNTFCVTCENQAP 95
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Gerbillinae,
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Zhang J., Dyer K.D., Rosenberg H.F.;
Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
EMBL. AR23834; AA67694.1; -.
HSSP: Plo153; IHIZ.
GO, GO:0003676; F:nucleic acid binding; IEA.
InterPro. DR001427; R:nacleic ribonuclease activity; IEA.
Pfam; PR00074; rnaseA.
Pfam; PR00074; rnaseA.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               21.1%; Score 122; DB 11; Length 157; 29.2%; Pred. No. 3.4e-06; tive 19; Mismatches 33; Indels 28
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PRINTS; PR00794; RIBONUCLEASE.

ProDom; PD000535; RNaseA; 1.

SMART; SM00092; RNASe Pc; 1.

PROSITE; PR00127; RNASE PANCEATIC; 1.

SRQUENCE 157 AA; 11945 MW; FDFE22FE77FE371A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Essinophil-associated ribonuclease 25.
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                       157 AA
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                          PRT;
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SEQUENCE FROM N.A.
MEDLINE=20243759; PubMed=10758160;
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Best Local Similarity
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SEQUENCE FROM N.A.
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NCBI_TaxID=10047;
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                                                                                                                                                                                                                               Length 157;
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Prodom; PD000535; RNaseA; 1.
SWART; SM00092; RNAse Pc; 1.
PROSITE; PS0127; RNASE PANCREATIC; 1.
SEQUENCE 157 AA; 17887 WW; 34FE2AE777EF3709 CRC64;
                                                                              21.1%; Score.122; DB 11;
29.4%; Pred. No. 3.4e-06;
iive 21; Mismatches 36;
                                                                                           Local Similarity
hes 32; Conservative
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Search completed: May 7, 2004, 21:46:01 Job time: 29.5753 secs

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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
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NCBI_TaxID=8355;
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Best Local Similarity
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les 39; Conserv
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Q9W738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 78288642, AAG30414.2; -.
HSSP, P11916, 1804.
GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                           MEDLINB=21599506; PubMed=11683320;
MSDLINB=21599506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38 (2001).
BENBL; AF351208; AR30254.1;
HSSP; P11916; 1BC4.
GO; GO:0004522; F:pancreatic acid binding; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                               kana catesbelana (bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 VLTTFEFYLSDCN----VTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95D61760F729868E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MRR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasell ribonuclease precursor.
Rana catesbeiana (Bull frog)
                                                                                                    01-JUN-2001 (TYEMBLrel. 17, Last sequence update) 01-OCT-2003 (TYEMBLrel. 25, Last annotation update) RNase A-type ribonuclease rc204 precursor. Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.3%; Score 274; DB 13;
47.7%; Pred. No. 7.1e-24;
tive 14; Mismatches 36;
                                             132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28:4097-4104(2000).
                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 22 P
132 AA; 14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Conservative
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catesbeiana (bullfrog)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                             Q98SM1;
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                                         098SM1
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Matches
RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 FOKKHLINI-RDVDCN-----NILSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                 DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LITFEFYLSDCNV---TSRP--CKYKLKKSINTFCVTCENQAPVHFVG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: |:|| : | :|| | | | | | :: | SKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinoshita N., Kirschner M.W.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF159166; AAD41901.1; -. HSSP; P00656; LLSQ. GO; GO:0003676; F:nucleic acid binding; IEA. GO; GO:004522; F:pancreatic ribonuclease activity; IEA. InterPro; IRRO142; RNaseA. PF00074; rnaseA: 1.
                                                                                                                                                                                         1 21 POTENTIAL.
22 132 RC-RNASEL1 RIBONUCLEASE.
132 AA; 14625 MW; D8D9AS17452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000635; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 1889I MW; D969F3E43B3CEIB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                       46.5%; Score 269.5; DB 13; 43.2%; Pred. No. 2.4e-23; ative 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%; Score 153.5; DB 1.36.1%; Pred. No. 8.3e-10; iive 19; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 AA.
Interpro; IPR001427; RNBSEA.
Pfam; PF00074; rnaseA; 1.
Prolom, PD000535; RNBSEA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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RESULT 14

Sat May

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8 17:57:22 2004

VLSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132

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QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                         MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
HEMBL; AF351210; AAK30256.1; -.
HESSP; P11916; 18C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana catesbeiana (Bull frog).

Eukaryota, Metazoa, Glordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura; Neobatrachia, Ranoidea, Ranidae, Rana, NCBI_TaxID=8400;
                                                                                                                                         Euteleostomi;
Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 VLTTFEFYLSDCN---VTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 22 POTENTIAL.
133 AA; 14615 MW; C8785B236B26E54E CRC64;
                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea,
                                                           (TremBlrel. 17, Created)
(TremBlrel. 17, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.4%; Score 280; DB 13;
46.8%; Pred. No. 1.4e-24;
tive 17; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AA
                                                                                                            RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bullfrog, Rana catesbeiana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Evol. 53:31-38(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 46.8
nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                           NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
                                                             01-JUN-2001 (
01-JUN-2001 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                               61S860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q98SM2
                            Q98SL9
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVRAICNG-VTNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 VLTTFEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 VLSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL 1 22 POTENTIAL.
SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                    RC-RNASE7.
131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) RNase A-type ribonuclease rc218 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                 48.2%; Score 279; DB 13;
46.8%; Pred. No. 1.9e-24;
tive 14; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00074; rnsseA; 1.
ProDom; PD000535; RNsseA; 1.
SMART; SMO092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
ProDon; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
EMBL; AF351207; AAK30253.1; -. EMBL; AF359578; AAL87036.1; -. HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                               14412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                             1
23
132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    L Similarity
52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                             CHAIN
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Q98SL8
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Wang S.-C.;

09DFY7

RESULT 5

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1 QDWLIFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ÓDWDTFOKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ODWLIFQKKHLINIRDVDCNNILSTNLF----HCKDKNIFIYSRPEPVKALCKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21539506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Indiangual diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana."; J. Mol. Evol. 53:31-38(2001). EMBL; AF351209; AAK30255.1; -BSSP, P11916; 18C4. GO; GO:0003676; F:nucleic acid binding; IEA. GO; GO:0004522; F:pancreatic ribonuclease activity; IEA. InterPro; IRO01427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0598M0;

01-JUN-2001 (TrEMBLrel. 17, Created)

01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

RNase A-type ribonuclease rc208 precursor.

RNase A-type ribonuclease rc208 precursor.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                        52.3%; Score 303; DB 13; Length 128; 52.9%; Pred. No. 3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.4%; Score 292; DB 13; Length 133; 48.6%; Pred. No. 5.9e-26; ive 16; Mismatches 33; Indels
                                                                     TISSUE=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AAG31442.2; -. HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                       GO; GO:0005676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPRO01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                         23 POTENTIAL.
128 RC-RNASE6 RIBONUCLEASE.
14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
87FCF122C3499E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
              Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 P
14628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       1
24 1
128 AA;
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Best Local Similarity
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                      Signal.
SIGNAL
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              REL
REP
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kana catespelana (BULL Irog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-Z0512555; Pubmed=11058105; Liao Y.D., Wei C.W., Tang P.C., Wang S.C.; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; Purification and cloning of cytotoxic ribonucleases from Rana catebbeina (bullfrog)."; Catebbeina (bullfrog)."; Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver,
MEDLINE-20512555, PubMed=11058105,
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                                                                      84 DEFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 DAFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR01427; RNaseA.
Pfam; PF00074; rnaseA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
RC-RNASE3 RIBONUCLEASE.
2 2814986082E0587D CRC64;
                                                               FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea,
NCBI_TaxID=8400,
                                                                                                                                                                                                                                         C1-MAR.2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasa3 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ol-WAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.7%; Score 305; DB 13; 53.8%; Pred. No. 1.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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128 AA; 14517 MW;
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HSSP; P22069; 10NC.
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                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                       24
                                                               61
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Q9DFY5;
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1 QDWIJFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                 23 PC
129 RC
14724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 R
14839 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001427; RNaseA.
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Matches 69; Conservative
                                                                                                                                                                                                                                                                                            69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bullfrod)
                                                                                                                                                                                                  1
24 1
129 AA;
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                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catesbeiana
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SIGNAL
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                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                     Signal.
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1 ODWLIFQKKHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                             Rana pipiens (Northern leopard frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20515555, PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 547; DB 13; Length 1:
Pred. No. 1.7e-55;
3; Mismatches 3; Indels
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                                                                SEPYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A39035; A39035.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                              Lião Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 953F90D351CFEEF3 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                          127 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 127 AA; 14469 MW;
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ProDom; PD000535; RNaseA; 1.
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SIGNAL
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Q9DFY6
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EMBL, AF242553, AAG31439.1;
-DBJ, 1MS9, 09-GMP.
GO, GO:0004527; F:pancheic acid binding; IEA.
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Indels
                                           POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                                                                                                                                                                                                                                                                                                                RC-RNASE4 RIBONUCLEASE.
826A62882B10ABDA CRC64;
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7, 2004, 21:29:10 ; Search time 29.5753 Seconds (without alignments) 1109.503 Million cell updates/sec
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1 QDWLFFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 20	878160	Q918VB;	01-0CT-2000	01-0CT-2000	01-0CT-2003	Onconase variant rapLR1 precursor.	Rana pipiens (Northern leopard frog).	Eukaryota; Metazoa; Chordata: Craniara: Vertehrata:	Amphibia, Batrachia, Anura: Neobatrachia: Ranoidea:	NCBI TaxID=8404;	[1]	SEQUENCE FROM N.A.	TISSUE=Liver;	MEDLINE=20330357; PubMed=10871370:	Chen SL., Le SY., Newton D.L., Maizel J V Jr Byhal S M	"A gender-specific mRNA encoding a cytotoxic ribonnolease	3' UTR of unusual length and structure ":	Nucleic Acids Res. 28:2375-2382(2000)	EMBL; AF165133; AAF76935,1;	PIR; A39035; A39035.	HSSP; P22069; 10NC.	GO; GO:0003676; F:nucleic acid binding; IFA	30; GO:00045	InterPro; IPR001427; RNaseA.	Pfam; PF00074; rnaseA; 1.	ProDom; PD000535; RNaseA;	SMART; SM00092; RNASe Pc; 1.	PROSITE; PS0	Signal.	SIGNAL	SEQUENCE 13		Query Match Best Local Similarity	Matches 102; Conservative	
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1 QDWLTFQKKGHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60

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; ORGANISM: Rana pipiens US-09-961-400-2

Query Match
46.8%; Score 281.5; DB 10; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps

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Search completed: May 7, 2004, 21:51:57 Job time: 35.2947 secs

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Sequence 2, Application US/09961400

Sequence 2, Application US/09961400

Sublication No. US20030124131A1

SEDERAL INCORMATION:
APPLICANT: STRAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 60/079-751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751
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                                 68 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1 OTHER INFORMATION: Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

98.0%; Score 590; DB 10; Length 110;
Best Local Similarity 97.3%; Pred. No. 2.2e-59;
Matches 107; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                           APPLICANT: Newton, Dianne 1.

APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
SROFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
MUMBER OF SEQ ID NOS: 43
LENGTH: 110
                                                                                                                                                                                  ; Sequence 19, Application US/09948391A; Publication No. US20030027311A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                           APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                            US-09-948-391A-19
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APPLICANT: RYBAK, SUGANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR PILING DATE: 2000-08-17

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PALENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Rana CHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
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TITLE OF INVENTION: Recombinant Anti-Tumor RNase FILE REFERENCE: 015280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT PILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: W6 06/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR PILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
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98.2%; Pred. No. 4.9e-60;
tive 2; Mismatches 0;
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Best Local Similarity 98.2°
Matches 108; Conservative
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Best Local Similarity 98.2
Matches 108; Conservative
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RESULT 12
US-09-948-391A-22
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                      61 STTRFQLNTCTRTSITPRPCPXSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Sequence 21, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: The United States of America

APPLICANT: The United States of America

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

TITLE REFERRICE: 015280-343110US

CURRENT FILING DATE: 1290-03-25

PRIOR FILING DATE: 1999-03-27

PRIOR FILING DATE: 1999-03-26

SPRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                         APPLICANT: Newton, Dianne M.
APPLICANT: Newton, Dianne D.
APPLICANT: Newton, Dianne D.
APPLICANT: Newton, Dianne D.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-3431100S
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PAPENTING NOWER: 2.00
SEQ ID NO 17
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Best Local Similarity 99.1%; Pred. No. 4.6e-60;
Matches 109; Conservative 0; Mismatches 1;
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ORGANISM: Artificial Sequence
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US-09-948-391A-21
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                       CTHER INFORMATION: Description of Artificial Sequence:Rana in OTHER INFORMATION: catesbelana ribonuclease with Met at position 1, OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant transfer INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
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                                                                                                                                                                          Length 111
                                                                                                                                                                                                                0; Indels
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Fublication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybar, Susanna M.
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
                                                                                                                                                                      Query Match
99.0%; Score 596; DB 10;
Best Local Similarity 98.2%; Pred. No. 4.6e-60;
Matches 108; Conservative 2; Mismatches 0;
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Rana catesbeiana
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Best Local Similarity
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Sequence 26, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
                                                                                                                APPLICANT: RYBAK, SUSANNA M.
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US-09-961-400-26
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ORGANISM: Rana catesbeiana
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Best Local Similarity 98.2
Matches 108; Conservative
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OTHER INFORMATION: Description of Artificial Sequence:Rana
CTHER INFORMATION: catesbeiana ribonuclease with Met at position
OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26
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99.2%; Score 597; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 109; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Fublication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Rewton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
FRIOR FILING DATE: 1998-02-05-10
FRIOR FILING DATE: 1998-03-26
FRIOR APPLICATION NUMBER: WS 09/622,613
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 2000-08-17
                                                                                                                                                                                                                                                                                                                                                                   Query Match

99.2%; Score 597; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 109; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                     ; ORGANISM: Rana catesbeiana
US-09-961-400-24
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US-09-948-391A-26
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TYPE: PRT
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RESULT 7 US-09-961-400-26

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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: MEMTON, DIANNE L.
TITLE OF INVENTION: TELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PRILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE PATENTIN VOY: 2.1
SEQ ID NOS: 43
LENGRAL 111
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US-09-561-400-19

i Sequence 19, Application US/09961400

j Sequence 19, Application US/09961400

j GENERAL INFORMATION:

j APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: REWTON, DIANNE L.

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/108

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/25

PRIOR FILING DATE: 2000-09-17

PRIOR FILING DATE: 1999-03-25

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR SPELICATION NUMBER: EQ/079,751

PRIOR SPELICATION NUMBER: 60/079,751

PRIOR SPELICATION NUMBER: 60/079,751

PRIOR SEQ ID NOS: 43

SOFTWARE: PATENTIN VOY: 2.1

LEMATH: 110
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99.2%; Score 597; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 109; Conservative 0; Mismatches 0;
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Length 111;

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DB 10;
                     100.0%; Score 602; DB 10;
100.0%; Pred. No. 9.6e-61;
tive 0; Mismatches 0;
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; Publication No. US20030124131A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                     Query Match
Best Local Similarity 100.
Matches 110; Conservative
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US-09-961-400-24
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US-09-948-391A-24
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| Sequence 17, Application US/09961400 |
| Publication No. US20030124131A1 |
| GENERAL INPORMATION: |
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: NEWTON: DIANNE L. |
| TITLE OF INVENTION: CELLS |
| FILE REFERENCE: 018733/1059 |
| CURRENT APPLICATION NUMBER: US/09/961,400 |
| CURRENT APPLICATION NUMBER: US/09-25 |
| PRIOR FILING DATE: 2000-09-25 |
| PRIOR FILING DATE: 1999-03-26 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: Patentin Ver: 2.1 |
| SEG ID NO 17 |
| TENNICE APPLICATION NUMBER: OF TABLES |
| SOFTWARE: Patentin Ver: 2.1 |
| SEG ID NO 17 |
| SEG ID NO 17 |
| SEG ID NO 17 |
| CONTRACT |
| CONTRA
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APPLICANT: GOLDENBERG, DATU M.
APPLICANT: GOLDENBERG, DATU M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: 05/62,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTION NUMBER: 60/079,751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTION NUMBER: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 15
LENGTH: 110
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Best Local Similarity 100.0%; Pred. No. 9.5e-61; Matches 110; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
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; ORGANISM: Rana catesbeiana
US-09-961-400-17
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US-09-961-400-15
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: OGLOENBERG, DAVID M.
TITLE OF INVENTION: INMUNICONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
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                                                                            2 QNWATEQQKHIINTPIICUTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINMAVL 61
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                                                    1 QNWATFOOKHIINTPIICHTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVL
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Gaps
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  Indels
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GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 43
SOFTWARR: Patentin Ver. 2.0
SEQ ID NOS: 43
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Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 109; Conservative 0; Mismatches 0;
        0
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OM protein - protein search, using sw model Run on:

7, 2004, 21:29:40 ; Search time 35.2947 Seconds May

(without alignments) 865.070 Million cell updates/sec

US-09-961-400-15

602 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters: 1140673 seqs, 277566755 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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(cgn2_6/prodata/2/pubpaa/US06 PUBC WBF PUB.pep:*
(cgn2_6/prodata/2/pubpaa/US06 PUBCOMB.pep:*
(cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/PCUGS PUBCOMB.pep:*
(cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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(cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
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(cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
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(cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*
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(cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
(cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:* Published_Applications_AA:* 5: 76: 10: 110: 112: 113: 114: 115: 117: 116:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description Sequence 15, Sequence 24, Sequence 24, Sequence 24, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 19, Sequence 21, Sequence 21, Sequence 21, Sequence 21, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22, Sequence 22,	19, Appi 2, Appli
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281.5	281.5	281.5	281.5	280.5	278.5	277.5	276.5	276.5	276.5	276.5	275.5	275.5	275.5	272.5	272.5	269.5	266.5	266.5		206	206	163	135.5	131.5	131.5	121	117.5	717	111	777	114.5
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ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbelana oocyte ribonuclease (RaCOR1) synt); OTHER INFORMATION: gene modified to use E. coli preferred codons US-09-948-391A-15
                                                        GENERAL INCORPATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
SOFWWARE: Patentin Ver. 2.0
SEQ ID NO 15
FENDING ALEMATINA NUMBER: US 08/622,613
SEQ ID NO 15
FENDING ALEMATINA VARIER IN THE SEQ ID NO 15
Sequence 15, Application US/09948391A Publication No. US20030027311A1
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ORGANISM: Artificial Sequence
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1 ONWAIFQOKHIINTPIICNTIMDNNIXIVGGOCKRVNTFIISSATTVKAICTGVINMANVL 60 Gaps Query Match
100.0%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.5e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0

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; ORGANISM: Rana pipiens US-09-961-400-9
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Query Match
Best Local Similarity 49.5%; Pred. No. 7.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps

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Search completed: May 7, 2004, 21:51:58 Job time: 35.2947 secs

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WS-09-961-400-9

Sequence 9, Application US/09961400

Publication No. US20303124131A1

Sequence 9, Application US/09961400

Publication No. US20303124131A1

SEQUENCE INVENTION: US20303124131A1

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: US-25

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 2000-08-17

PRIOR PEDICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENT NOS: 43
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98.3%; Score 590; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 5e-59;
Matches 107; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                 GENERAL INFORMATION

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

ITILE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REPERENCE: 015280-34311008

CURRENT APPLICATION NUMBER: US/09/948,391A

FRIOR APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1998-03-26

PRIOR PRIOR DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR PRIOR DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR PRIOR DATE: 1998-03-26

PRIOR DATE: 1998-03-26

PRIOR DATE: 1998-03-26

PRIOR DATE: 1998-03-27

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PRIOR PRIOR DATE: 1998-03-27
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LENGTH: 11
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Sequence 26, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 000-09-25

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 1900-03-26

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

SOFTWARE: PALCHIN VOR: 2.1
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98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels
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APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Recombinant Anti-Tumor RNase; FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: WG 96/22,613
PRIOR PILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.5%; Score 591; DB 10;
98.2%; Pred. No. 3.9e-59;
tive 2; Mismatches 0;
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Best Local Similarity 98.2'
Matches 107; Conservative
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US-09-961-400-26
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 110
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                                                                                                                                                    FEATURE:
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       2 QNWAJFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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                                                                                             62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RaCORI OTHER INFORMATION: Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110;
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of the APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
                                                                                                                                                                                                                                                                                                                              APPLICANT: Myewron, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311005
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WG 60/079,751
PRIOR FILING DATE: 1999-03-27
PRIOR PLICATION NUMBER: WG 09/622,613
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%; Score 594; DB 10;
99.1%; Pred. No. 1.7e-59;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                   Sequence 19, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rybak, Susanna M.
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US-09-948-391A-24
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GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
PITLE OF INVENTION: DIANNE L.
TITLE OF INVENTION: CELLS
FILE REFERENCE: 01873/1059
CURRENT APPLICATION NUMBER: 08/09/61,400
CURRENT FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: PCT/US99/06641
PRIOR PAPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PELING DATE: 1998-03-26
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                                                                                          CTHER INFORMATION: Description of Artificial Sequence:Rana
CTHER INFORMATION: catesbelana ribonuclease with GlnlSer substitution
CTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                            Length 110;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Best Local Similarity 98.2%; Pred. No. 3.8e-59;
Matches 107; Conservative 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 98.23
Matches 107; Conservative
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: INMUNER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-09-17
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALENTING DATE: 1999-03-26
SEQ ID NOS: 43
SOFTWARE: PALENTING DATE: 1999-03-26
SEQ ID NOS: 43
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| Publication No US20030124131A1
| GENERAL INRORANTAION:
| APPLICANT: RYBAK, SUSANNA M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: MANTON DIANNE L.
| TITLE OF INVENTION: IMMOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT ITLE OF INVENTION: IMMOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT ITLE OF INVENTION: UMBER: US/09/961,400
| TITLE OF INVENTION: CELLS
| FILE REFERENCE: 018733/1059
| CURRENT FILING DATE: 2001-09-25
| FRIOR APPLICATION NUMBER: 09/622,613
| PRIOR FILING DATE: 1999-03-26
| PRIOR PILING DATE: 1999-03-26
| PRIOR PILING DATE: 1998-03-26
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE E PATENTIN VET. 2.1
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98.2%; Pred. No. 1e-59;
Live 2; Mismatches
                                                       US-09-961-400-15
Sequence 15, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rana catesbeiana
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Matches 108; Conservative
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Fublication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Newton, Dianne M.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Bepartment of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RASSE

TITLE OF INVENTION: Recombinant Anti-Tumor RASSE

TITLE OF INVENTION: Recombinant Anti-Tumor RASSE

CURRENT APPLICATION NUMBER: US/09/948,391A

CURRENT FILING DATE: 1999-03-27

PRIOR FILING DATE: 1999-03-27

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR FILING DATE: 1999-03-26

PRIOR PELLING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VOR: 2.0
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Pred. No. 3.9e-60;
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CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR PPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN PAT: 2.1
                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 110; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                 ORGANISM: Rana catesbeiana
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                                                                                                                                                                                                                                                                                                       ; OKGANISM: KAI
US-09-961-400-22
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                                                                                                                                                                                                                                                                           TYPE: PRT
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US-09-961-400-22
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US-09-961-400-21
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Sequence 210. Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: OCLDENBERG, DAVID M.
APPLICANT: NEWTON DIANNE L.
TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CLLS.
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QNWAIFQQKHIINIPIICNTILDNNIYIVGGQCKRVNFFIISSAITVKAICTGVINLAVL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: catesbelana ribonuclease with Met at position 1, INFORMATION: Met23Leu and Met58Leu substitutions (recombinant INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 STTREQLNTCTRISITPRPCPYSSRTETNYICVKCBNQYPVHFAGIGRCP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Rana
                                                                                                                                                                                                                                                                                                                   APPLICANT: Nyder, Sugaria in Applicant: Applicant: Applicant: The United States of America Applicant: Department of Health and Human Services TITLE OF INVENTION: Recombinant Anti-Tumor RNase TITLE REFERENCE: 015280-343110US CURRENT APPLICATION NUMBER: US 60/079,751 CURRENT FILING DATE: 1938-03-27 PRIOR APPLICATION NUMBER: WO PCT/US99/06641 PRIOR FILING DATE: 1939-03-26 PRIOR FILING DATE: 1939-03-26 PRIOR FILING DATE: 2000-08-17 NUMBER OF SEQ ID NOS: 43 SOFTWARE: PARCH PRIOR P
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PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 2000-08-17
PRIOR PLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                 Sequence 21, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                               APPLICANT: Rybak, Susanna M.
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Best Local Similarity 100.
Matches 110; Conservative
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LENGIH: 111
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Publication No. US20030124131A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: REAK, SUSANNA M.
APPLICANT: OOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
                                                                                                     1 ONWATEQOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions OTHER INFORMATION: (recombinant Met(-1) RACORI Met22Leu Met57Leu-(His)6)
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Length 111;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Wybak, Susanna L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Bepresented by The Secretary of the
APPLICANT: Department of Health and Human Services
TILLE REFERENCE: 018280-34311005
CURRENT APPLICATION NUMBER: US 09/948,391A
CURRENT FILING DATE: 2002-05-10
FRIOR PILING DATE: 1998-03-27
FRIOR APPLICATION NUMBER: W0 PCT/US99/06641
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
SRIOR APPLICATION NUMBER: W1 09/622,613
FRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
100.0%; Score 600; DB 10;
100.0%; Pred. No. 3.7e-60;
iive 0; Mismatches 0;
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, Sequence 22, Application US/09948391A
, Publication No. US20030027311A1
, GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 110; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May Run on:

7, 2004, 21:29:40 ; Search time 35.2947 Seconds (without alignments) 865.070 Million cell updates/sec

US-09-961-400-19 Title: Perfect score:

Sequence:

1 QNWATFQQKHIINTPIICNT......ICVKCENQYPVHFAGIGRCP 110

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

1140673 segs, 277566755 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	19,	Sequence 21, Appl Sequence 21, Appl	22,		12,0	17,	13,	4.		0 0	0,1	Sequence 1/, Appl Sequence 9. Appli
SUMMARIES	US-09-961-400-19	US-09-961-400-21	US-09-948-391A-22 US-09-961-400-22	US-09-948-391A-15	US-09-961-400-15	US-09-961-400-17	US-09-948-391A-19	US-09-961-400-24	US-09-948-391A-26	US-09-961-400-26	US-09-948-391A-17	US-09-961-400-9
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Sequence 9, Appli

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equence 2 equence 6 equence 6	3004	Sequence 4, Appli Sequence 8, Appli Sequence 2, Appli Sequence 11, Appl Sequence 11, Appl	निसं तनक	m	Sequence 89, Appl Sequence 139, Appl Sequence 141, Appl Sequence 254, Appl Sequence 254, Appl Sequence 58, Appl Sequence 58, Appl
US-09-961-400-2 US-09-948-391A-6 US-09-961-400-6 US-09-961-201A-20	US-09-961-400-28 US-09-961-400-28 US-09-948-391A-2 US-09-948-391A-4	US-09-961-40 US-10-153-88 US-09-948-39 US-09-961-40	Þ	US-09-948-391A-9 US-10-461-713-53 US-09-986-119-3 US-09-918-887-3 US-10-016-447-2 US-10-037-417-103	-016-248-8 -074-978A- -074-978A- 731-872-25 -876-997-2 -461-713-5
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ALIGNMENTS

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Sequence 19, Application US/09961400
| Sequence 19, Application US/09961400
| Publication No. US20030124131A1
| GENERAL INPORMATION:
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: WENTON: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT ITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT ITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT |
| TILLE OF INVENTION: CELLS |
| TILLE OF INVENTION: 1873/1059 |
| CURRENT APPLICATION NUMBER: 09/622,613 |
| PRIOR FILING DATE: 2001-09-25 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR APPLICATION NUMBER: 60/079,751 |
| PRIOR APPLICATION NUMBER: 60/079,751 |
| PRIOR APPLICATION NUMBER: 60/079,751 |
| PRIOR PRIOR APPLICATION NUMBER: 60/079,751 |
| PRIOR ELING DATE: 1998-03-26 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE PARCENTIN OF 12.
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ORGANISM: Rana catesbeiana
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RESULT 1
US-09-961-400-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ATPQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFILSSATTVKALCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 19 POTENTIAL.
20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;
                                                                                                                                                                                                                                                                Tragulus javanicus (Lesser Malay chevrotain).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
Tragulidae; Tragulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 21.8%; Score 131; DB 6; Length 170; 1 Similarity 33.1%; Pred. No. 2.8e-07; 41; Conservative 17; Mismatches 46; Indels :
                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO: GO:0004519; F:endonuclease activity; IEA.
GO: GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AA.
                                          170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Endonuclease; Hydrolase; Nuclease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGM, PE00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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ANG4.
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Q80Z85
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                   Q9BEC1
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33 CKRVNTFIISSATTVKAIC---TGVINMAV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE
Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I., "Angiogenins: a new class of microbicidal proteins involved in innate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.3%; Score 128.5; DB 11; Length 144; Best Local Similarity 38.2%; Pred. No. 4.6e-07; Matches 29; Conservative 13; Mismatches 29; Indels 5;
                                                                                      Nat. Immunol. 4:269-273 (2003).
EMBL, AY219870; AAO62354.1; -
GO, GO:0003676; F:nucleic acid binding; IEA.
GO, GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                            Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SROUDO: 144 AA; 16554 MW; 09808807C00224C1 CRC64;
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122 FRYIVIACEDGWPVHF 137
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FRL2 protein.
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Q9W738;
                                                                                                                                              Signal.
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                                                                                                                                                                 SIGNAL
                                                                                                                                                                                     CHAIN
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Q9W738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242556, AAG31442.2; -. HSSP, P22069; JONG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Gaps
                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana,
NCBI_TaxID=8400;
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Rrana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordaca; Craniata; Vertebrata; Buteleostomi;
Amphibla; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                              MEDLINE=20512555, PubMed=11058105, Islao Y.D., Huang H.C., Leu Y.J., Mei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog)...;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.6%; Score 226.5; DB 13; Length 128;
41.1%; Pred. No. 1.5e-18;
tive 18; Mismatches 39; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 28:4097-4104 (2000).
BMBL; AF245554; AAG31440.2;
HSSP; P22069; 10NC.
GO; GO:0004575; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC-RNASE3 RIBONUCLEASE.
2B14986082E0587D CRC64;
                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                               128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 AA
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Nucleic Acids Res. 28:4097-4104(2000).
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                          RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Bull frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 128 R
128 AA; 14517 MW;
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ProDom; PD000535; RNaseA; 1.
                                        PRELIMINARY;
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128
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Best Local Similarity
'hne 46; Conserve
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Q9DFY5;
                                        Q9DFY7
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RESULT 11
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                     Q9DFY7
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96069863; PubMed=7585965;
Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a Yeast screening method and their activity in Xenopus development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryots, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 STEVISKELLPLIDČLLMGRIARPPNČAŽNOTRTIGVINITČENNÝPVHFAG 138
                                                                                                                                                                                                                                                                                                                  6;
                                                                                                                                                                                                                                                             36.1%; Score 217.5; DB 13; Length 128; 39.3%; Pred. No. 1.7e-17; tive 19; Mismatches 40; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 MN-VLSTTRFQLNTCTRISITPRP--CPYSSRTEINYICVKCENQYPVHFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF159166; AA041901.1; -.
HSSP; P00656; LisQ.
GG) GC:0003676; F:nucleic acid binding; IEA.
GG) GC:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; PR00147; RNASEA.
PFODOM; PD000535; RNASEA.
PPODOM; PD000535; RNASEA.
RROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3B43B3CE1B8 CRC64;
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
                                                                                                                                                                   1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.1%; Score 163; DB 13;
39.3%; Pred. No. 5.2e-11;
ive 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 AA
                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                           Query Match
Best Local Similarity

2...
44; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 39.34 es 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                SEQUENCE
                                                                                                     Query Match
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                                                Signal.
SIGNAL
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                                                                                                                                                                                                                                                                              Q9DFY8
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                                                                     CHAIN
                                                                                                                              Matches
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                                                                                                                                                                                                                                                                   Q9DFY8
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EMBL, AF242555, AAG31441.2; --
PDB; IKVZ; 28-JUL-02.
                                                                                                                                                                                                                                                                                                                                                                                                              1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                  24 ODWLTFOKKHITNIRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE-20512555; PubMed-11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbelana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTTSEFYLSDC---NVTSRPCKXKLKKSTNKFCVTCENQAPVHFVGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                46.1%; Score 277.5; DB 13; Length 127; 49.5%; Pred. No. 1.7e-24; tive 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
                                                                                                                                                                                                   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332139; AAL54383.1; -.
                                                                                                                                                                                                                           PIR; A39035; A39035.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
Interpro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                            127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Tremblrel. 16, Created)
(Tremblrel. 18, Last sequence update)
(Tremblrel. 25, Last annotation update)
                                                                        Last annotation update)
                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AA
                              127 AA.
                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                           [1]
SEQUENCE FROM N.A.
Liao Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
"Rana pipiens onconase genomic GNA.";
                                                                                                            Rana pipiens (Northern leopard frog)
                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                               PRT;
                                                                                                                                                                                                                                                                                   ProDom; PD000535; RNaseA; 1.
                                                    01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                        Onconase precursor.
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8400;
                                                                                                                                           NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                          55;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9DFY6;
                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                          Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DFY6
                               QBUVX5
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
          RESULT 8
                   Q8UVX5
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                                                                                                                                                                                                                                                                                             1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                             24 QDWATFKKKHLTDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF242553; AAG31439.1; -.

PDB; IMS8; 09-JAN-03.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:nucleic acid binding; IEA.

InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   59 VLSTTRFQLNTCTRISITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 VLSTTREQLNTCTRISITERPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 VLSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 128;
                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                80 VISNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELFVHFAGVGICP
                                                                                                                                                                                             Length 129;
                                                                                                                                                                40.9%; Score 246; DB 15,
40.9%; Score 246; DB 15,
*.. Pred. No. 8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.1%; Score 229.5; DB 13; Length 40.2%; Pred. No. 6.7e-19; tive 20; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 23 POTENTIAL.
24 128 RC-RNASE2 RIBONUCLEASE.
128 AA; 14839 MW; 989719CF52053ECC CRC64;
                                                                                                                     RC-RNASE4 RIBONUCLEASE.
826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                        1 Similarity 43.4%; Pred. No. 8e-2149; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00074; rnaseA; 1.
ProDon; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                  POTENTIAL.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Last a
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                  1 23 PC
24 129 RC
129 AA; 14724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Conservative
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                                                                                                                                                                                                                             Local Similarity
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Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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th 62.5%;
| Similarity 65.8%;
73; Conservative 9
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                       22
132 AA;
  P11916; 1BC4.
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                   SEQUENCE
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                                                                                                                                                            Query Match
                                                                                               Signal.
SIGNAL
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SIGNAL
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 HSSP;
                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                       RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ONWATFOOKHIINTPII-CHTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang P.-C., Wang S.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrENBLrel. 16, Created)
01-OCT-2001 (TrENBLrel. 18, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
RC-RNaseL1 ribonuclease precursor.
Rana catesbelana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia, Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbelana (bullfrog).";
Catesbelana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF288642; AAG30414.2;
                                                                                                                                                                                                                                                                                                                                                                         1 22 POTENTIAL.
132 AA; 14704 MW; 95D61760F729868E CRC64;
                                                         01-07N-2001 (TrEMBLrel. 17, Created)
01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                             74.5%; Score 448.5; DB 1
78.2%; Pred. No. 1.9e-44;
                                          132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AA
                                                                                                                                                                                                                                                                                                                    Probom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                           Rana catesbeiana (Bull frog).
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
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Best Local S
                                                   Q98SM1;
                                                                                                                                                                                                                                                                                                                                                             Signal.
SIGNAL
                                     Q98SM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure.";
Wucleic Acids Res. 28:2375-2382(2000).
BMBL; AF165133; AAF76935.1;
PIR; A39035; A39035
HSSP; P22069; 10NC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 VLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 ELSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 VLSTTRRQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                          2;
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llarity 49.5%; Pred. No. 5.7e-25;
Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                             Score 376; DB 13; Length 132;
Pred. No. 5.6e-36;
9; Mismatches 27; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfan; PF00074; rnaseA; 1.
ProDom; PF000535; RNaseA; 1.
SWART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                            21 POTENTIAL.
132 RC-RNASEL1 RIBONUCLEASE.
14625 MW; D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Rana pipiens (Northern leopard frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA
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ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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SEQUENCE
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbelana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
Enkaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrazoia; Anuxa; Neobatrachia; Ranoidea; Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LSTTREQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                      83 LSTTRFQLNTCTRTSITFRECPYSSRTENNYICVKCENQYPVHFAGIGRCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 487.5; DB 13; Length 132; Pred. No. 5.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR01427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 22 POTENTIAL.
23 132 RC-RNASE7.
132 AA; 14412 MW; 131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOGT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AA.
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                                                                                                                                                                                                                                                         132 AA.
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SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                         PRT;
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83.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.",
J. Mol. Evol. 53:31-38(2001).
HMDI, PAT51210; AAK30266.1; -.
HSSP; P11916; 1BC4.
GO; GO:0004522; F:pancreatic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
Bull frog).
Bull frog).
Buraryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                      79.5%; Score 478.5; DB 13; Length 133; 78.4%; Pred. No. 6.2e-48; ive 11; Mismatches 12; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.3%; Score 471.5; DB 13; 76.6%; Pred. No. 4.1e-47; ative 13; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00074; rnaseA; 1.
ProDon; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                 Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF351211; AAK30257.1; --
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                22 PC
14615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
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OM protein - protein search, using sw model

7, 2004, 21:29:10 ; Search time 31.2816 Seconds (without alignments) 1109.503 Million cell updates/sec Run on:

US-09-961-400-15 Title: Perfect score:

602 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Sequence:

Scoring table:

1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_lungi:*
4: sp_lungi:*
5: sp_lungi:*
5: sp_lungi:*
6: sp_phame:*
7: sp_phage:*
7: sp_phage:*
7: sp_phage:*
7: sp_phage:*
7: sp_phage:*
7: sp_vordent:*
7: sp_vordent:* sp_rvirus:*
sp_bacteriap:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

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07YR.T6	08VD94	O9RDC2	09TVC0	ORVDAR	09RH14	O7VD.TE	OBE1VE	ORKOTO	OBCEGS	ORVDG2	086174	086173	ORGIVO	086177	21100	COUNTY	080756	0817095	Ogundo	ORVINGA	088005	080663	097V2B	0977730	000000	20000	CONTROL CONTROL	X 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	20200
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147	150	163	116	150	144	147	146	149	149	150	146	146	146	146	153	124	148	149	134	152	156	148	119	119	147	1 2 5	124	1 2 6	1
21.2	20.9	20.8	20.7	20.6	20.3	20.2	20.1	20.0	20.0	19.9	19.9	19.7	19.7	19.7	19.4	19.0	18.7	18.7	18.6	18.5	18.5	18.4	18.4	18.4	18.2	18.2			,
127.5	126	125.5	124.5	124	122.5	121.5	121	120.5	120.5	120	119.5	118.5	118.5	118.5	116.5	114.5	112.5	112.5	112	111.5	111.5	111	110.5	110.5	109.5	109.5	109	108.5	
17	18	13	20	21	22	23	24	52	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Buteleostomi; Ranidae; Rana. clease from th	Length 133; Indels 1:	
nicella sas	ength	1
.e) a; Eui a; Ran onucle		1
RELIMINARY; PRT; 133 AA. (TrEMBLrel. 17, Created) (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 25, Last annotation update) (TrEMBLrel. 25, Last annotation update) ana (Bull from and an annotation update) ana (Bull from an an an annotation and and an and an and an and an and an	DB 13; 7e-57; 3 5:	,
133 AA.) quence up notation cursor. cursor. ata; Vert achia; Ra achia; Ra ing; IEA. lease act lase act AI. AI.	60.5; o. 1.7 atches	
PRT; 1 Created) Last seque Last seque Last annot 208 precur .; Craniata Neobatrach ase A supe; id binding; ribonucles ribonucles ribonucles	Score 560.5; DB 1 Pred. No. 1.7e-57; 0; Mismatches 5	
NARY; rel. 17, Cr rel. 25, La rel. 25, La clease rc20 clease rc20 clordata; Anura; Ne ion of RNas sbeiana; 38(201). 10255.1; 10255.1; 1016ic acid nncreatic r: RNaseA; RA, RA RA RA, RA RA RA, RA	.,. * * 19	
PRELIMINARY; (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. Tribonucleas iana (Bull fracaca; Chorr Frachia; Anu 400; (N.A. 55.6; Pubmed 7., Zhang J., ification of ification of ification of a catesbeiar ARX30255. 187. 187. 187. 187. 187. 188. 21. 188. 22. 23. 24. 24. 25. 24. 25. 25. 25. 25. 26. 26. 26. 27. 27. 28. 28. 28. 28. 28. 28. 28. 28. 28. 28	vat	
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RESULT 1 O985M0 PRELIMINARY; PRT; 133 AA. D1 0985M0 PRELIMINARY; PRT; 133 AA. C 0985M0 PRELIMINARY; PRT; 133 AA. D2 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) O1 -JUN-2001 (TrEMBLrel. 25, Last sequence update) D2 01-JUN-2001 (TrEMBLrel. 25, Last sequence update) D3 Rana catesbeiana (Bull firog). C Amphibia; Batrachla; Anura; Neobatrachia; Ranoidea; Rana. NCB1 Tax1D=8400;	weer, march Best Local Similarity Matches 105; Conser	
RESULTATION OF THE PARTY OF THE	Mar	

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TELEPHONE: 718-625-0399
TELERA: 718-625-0399
TELERA: No. 5529775 Applicable
INFORMATION FOR SEQ 1D No. 1:
SEQUENCE CHARACTER.STICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORGANISM: ROMES
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
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g

Search completed: May 11, 2004, 14:37:53 Job time : 16.5747 secs

Query Match 45.0%; Score 272.5; DB 1; Length 104; Best Local Similarity 49.1%; Pred. No. 3.5e-24; Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps

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REFERENCE/DOCKET NUMBER: 5006 US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 49.1%
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-875-811-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.8%; Score 277.5; DB 3; Length 358; Best Local Similarity 49.1%; Pred. No. 4.2e-24; Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 NVLSTTRFQLNTCTRTSITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Rodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                       MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATPONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONEY/AGENT INFORMATION:
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APPLICATION UNDER: US/08/875,911 FILING DATE: 19-FFBE-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY. San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Faris, Susan K. REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 358 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
San Francisco
                        California
                                                              94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-875-811-26
                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
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1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
IITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 276.5; DB 3; Length 105;
49.1%; Pred. No. 1.2e-24;
tive 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                           015280-244100US
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-UUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                             US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                  FILING DATE: 19-FEB-199
FILING DATE: 19-FEB-199
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05 60/011.
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT TRFORMATION:
RAGISTRATION NUMBER: 41,739
REFREENCE/DOCKET NUMBER: 01521
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
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Patent No. 5529775
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us-09-961-400-26.rai

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1 MSNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Gaps
                                                                                                                 NVLSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 110
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49.1%; Pred. No. 9.4e-25;
tive 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                  Sequence 39, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCES: 64
CORRESPONDENCES: 64
CORRESPONDENCES: Canabara and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNATURE STATEMENT Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 3.35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REPERBNIC/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                           US-08-875-811-39
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RESULT 12 US-08-875-811-41

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251 MEDWIJFQKKHITNTRDVDCDNIMSTNIF----HCKDKNIFIYSRPEPVKAICKGIIASK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 277.5; DB 3; Length 355; 49.1%; Pred. No. 4.1e-24; Live 15; Mismatches 33; Indels 9
                                                                       APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rowton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF UNEWTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSITCATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUSAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: FALLS, - TREGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
(415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 41, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Conservative
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-875-811-51
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PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 576-0200
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 amino acids
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                    ; LOCATION: 1..355
; OTHER INFORMATION:
US-08-875-811-64
                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                 Query Match
Best Local Similarity
Lag 56; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                     linear
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ZIP: 94111-3834
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-875-311-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSDWLIFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                     46.5%; Score 281.5; DB 3; Length 355; 50.0%; Pred. No. 1.4e-24; tive 15; Mismatches 32; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rybak, Susamna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Hodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS: 64
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARES PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION POR SEQ ID NO: 64:
                                                                                       015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/08875811
Patent No. 6045793
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SHABI K.
REGISTRATION NUMBER: 41,739
REFERENCE/POCKET NUMBER: 0152:
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 355 amino acids
                                                                                                                                                                                                                 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.03
Matches 56; Conservative
                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-875-811-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-875-811-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                   307 NVLITSEFYLSDC----NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
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                                                                          Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Liuis
APPLICANT: Bodue, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
                                                                                                                                32; Indels
/note= "E6FB[Met-(-1)]SerrOnc"
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APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998
                                                                             46.5%; Score 281.5; DB 3; 50.0%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faxis, Susan K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
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Best Local Similarity
Matches 56; Conserva
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49, Application US/08875811
Patent No. 6045793
GENERAL INFORATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
UNMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE:
CLASSIFICATION: 435
                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Bubarcadero Center, Bighth Floor CITY: San Francisco GTAY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-875-811-61
                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                              STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                     USA
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                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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251 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 NVLTISEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SECUENCES: 64
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 60/011,800
FILING DATE: 19-FEB-1996
ATONNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/POCKET NUMBER: 41,739
REFERENCE/POCKET NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 281.5, DB 3
Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 56; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-875-811-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94111-3834
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147 MSDWLTFOKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
64 NVLITSEFYLSDC---NVISRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 281.5; DB 3; Length 2; Pred. No. 9.3e-25; 15; Mismatches 32; Indels
                                                                                                                                                                                                            APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodwer, Alexander
IIILE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015280-244100US
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CIASSIFICATION: 435
PRIOR APPLICATION 1435
APPLICATION DATE: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FATIS, SUSAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61, Application US/08875811;
Patent No. 6045793;
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
                                                                                                                                        ; Sequence 59, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41,739
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.5%;
Best Local Similarity 50.0%;
Matches 56; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-875-811-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-875-811-61
                                                                                                                         US-08-875-811-59
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                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                        3 NWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV 60
                                                                                                                                                                                                       2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
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                                                                                                                                                                                                                                                                    61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                               9,
                                                                                Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 112;
                                                                                                                            31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEADJABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
AMANDE DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%; Score 281.5; DB 3
50.0%; Pred. No. 3.5e-25;
iive 15; Mismatches 32
                                                                           46.6%; Score 282.5; DB 1.
50.0%; Pred. No. 2.4e-25;
tive 15; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 015280-244100US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41,739
            DEVELOPMENTAL STAGE: Occyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.01
Matches 56; Conservative
                                                                                                   Best Local Similarity 50.0
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Faris, Susan K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                   ;
US-08-467-955-2
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STATE:
                                                                                Query Match
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4;

Gaps

9

Length 251;

1; Gaps

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2 NWAIFQQKHIINTPIINCNIIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMAVL 61
                                                                                                                                                                                                    3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Mojciech J.
APPLICANT: Ardelt Ph.D, Mojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
                                                                                                                                                                                                                                                                                                                      62 STTRFQLNTCTRTSIIPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                             62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                   Score 586.5; DB 3; Length 111;
Pred. No. 1.9e-60;
0; Mismatches 0; Indels 1
  /note= "Frog Lectin from Rana
catesbeiana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
FILING DATE: 03-FEB-1992
FILING DATE: 01-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08467955
Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO. 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Mark H. Jay, P.A. STREET: P.O. BOX E CITY: Short Hills STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION: 201-912-9066
                                                                                                   Query Match
Best Local Similarity 99.1%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
    ) OTHER INFORMATION:
; OTHER INFORMATION:
US-08-875-811-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07078-0383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                            3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                Length 111;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Lluis B.
APPLICANT: Wlodawer, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                    LOCATION: 1..111

GOTHER INFORMATION: /note= "Frog Lectin from Rana
GTHER INFORMATION: catesbeiana"
US-08-891-848-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ELING DATE: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                           Query Match 96.8%; Score 586.5; DB 2;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Pater: PC-DOS/Ms.TCURPERME: Pater:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-875-811-8
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments)
345.738 Million cell updates/sec May 11, 2004, 14:33:03 ; Search time 16.5747 Seconds Run on:

606 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 US-09-961-400-26 Perfect score: Sequence:

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched: 389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents AA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ	•		SUMMARIES	
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No.	Score	Match	Length	B :	ID	Description
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7	586.5	σ	111	m	-08-875-811-	equence 8,
m	282.5		104	٦	-08-46	Sequence 2, Appli
4	281.5	4	112	æ	-08-875	32,
ហ	281.5	46.	251	m	-08-87	59
9	281.5	46.	254	m	-08	61,
7	281.5	46.	355	ĸ	-08-	49,
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D	281.5	46.	355	m	8	64,
10	281.5	4	366	m	US-08-875-811-55	
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22	272.5	45.0	104	4	US-09-687-748-1	H
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24	272.5	45.0	104	4	US-09-095-429-1	Sequence 1, Appli
25	272.5	45.0	104	4	US-09-986-119-1	'n
26	272.5	45.0	106	m	18-875-811-2	28
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Appl Appl Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli App	APPLL
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US-08-875-811-63 US-08-875-811-45 US-08-875-811-45 US-08-875-811-43 US-08-875-811-43 US-09-875-811-23 US-09-934-268-2 US-09-687-748-2 US-09-687-748-2 US-09-687-148-2 US-09-223-118-3 US-09-223-118-3 US-09-223-118-1 US-09-223-118-1	C-7/9-T/
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	40

## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM.TYPE: Floppy disk
COMPUTER: IBM PCCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 015280-110310US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 20-OKT-1991
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
FILING DATE: 20-APR-1990
                                                    ; Sequence 12, Application US/08891848 ; Patent No. 5955073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INPORMATION FOR SEO ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 111 amino acids
TYPE: amino acid
RESULT 1
US-08-891-848-12
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CKRVNTFIISSATTVKAICTGVINMNVLS	CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRS	
34	39	
ò	qq	

89 TNYICVKCENQYPVHF 104

ö Dp

99 FRTIAVACENGLPVHF 114

PARCEASIC Tibonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
N;Alternate names: RNase IB
N;Alternate names: RNase IB
C;Species: Gavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;Van den Bergy, A:; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases: Isolation, properties, primary structure a
A;Recession: A00826
A;Molecule type: protein
A;Recession: A08826
A;Molecule type: protein
A;Residues: 1-128 <AMN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His #status predicted
F;21,34/Binding site: carbohydrate (Ash) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

7 FOOKHI-----INTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV 60 Query Match 19.6%; Score 118.5; DB 1; Length 128; Best Local Similarity 31.6%; Pred. No. 8.7e-05; Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps

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Search completed: May 11, 2004, 14:37:08 Job time: 13.5611 secs

Db 6 AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCSQK 61 Qy 59 NVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104	RESULT 13 NRMS pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
62 NVACKNGQINCYQSYSIMSIIDCREIGSSKYPNCAYKTIQAKHIIVACBGNPYVPVHY	N.Alternate names: RNase 1, RNase A C,Species: Mus musculus (house mouse) C;Date: 30-Nov-1980 #sequence revision 13-Mar-1997 #text_change 18-Jun-1999
4-0ct-1996	C.R.CESSION: A34939; 522395; AUG830 R.Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J. Mol. Biol. Evol. 7, 29-44, 1990 A;Title: Evolution of nucleic acids coding for ribonucleases: the MRNA sequence of mouse A;Reference number: A34090; MUID:90136034; PMID:2299980 A;Accession: A34090
	A; Molecule type: mkNA A; Residues: 1-149 < SCH> A; Cross-references: GB: M27814; NID: 9200762; PIDN: AAA40060.1; PID: 9200763 R; Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H. Nucleic Acids Res. 19, 6935-6941, 1991
A;Molecule type: protein A;Residues: 1-122 <gaa> C;Superfamily: pancreatic ribonuclease C;Experfamily: pancreatic ribonuclease F;11,40,117/Active site: His, Lys, His #status predicted</gaa>	
	A;Cross_references: EMBL.X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982 R;Lenstra, J.A.; Beintema, J.J.  Bur. J. Blochem. 98, 399-408, 1979 A;Title: The amino acid sequence of mouse pancreatic ribonuclease. A;Reference number: A00830; MUID:80024269; PMID:556267
7 FORCHI STATEMENTY TOGGOCK TOTAL STATEMENT TO STATE	A.Molecule type: protein A.Residues: 26-149 <len> C.Superfamily: pancreatic ribonuclease C.Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas</len>
QY 53 TGVINMNVLSTTRFQLATCTRISITPRP-CPYSSRTETNYICVKCENQY-PVHF 104	Fil-25/Domain: signal sequence #status predicted <sig> Fi26-149/Product: parcreatic ribonuclease #status experimental <mat> Fi37,66,164/Active site: His, Lys, His #status predicted Fi51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted Fi62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></sig>
3.1.27.5) - nutria (tentative sequence)	Query Match Best Local Similarity 30.8%; Pred. No. 6.5e-05; Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;
NyALCETRATE NAMES: KNASE 1; KNASE A C;Species: Myocastor coypus (nutria, coypu) C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 C;Accession: A00822	QY 7 FQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
Rivan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Biochim. Biophys. Acta 453, 400-409, 1976 A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896	Qy 61 LSTTRFQLNTCTRISITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
Ayaccession: August Ayaolecule type: protein Ayasidues: 1-128 <van C:Superfamily: pancreatic riboniclesse</van 	RESULT 14
C; Keywords: glycoprotein, hydrolase; nucleic acid digestion, pancreas F;12, 41, 119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental	angiogenin - pig C.Species: Sus scrofa domestica (domestic pig) C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C.Accesion: S29834; A43825
Query Match Best Local Similarity 31.6%; Pred. No. 5.5e-05; Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;	R:Bond, M.D.; Strydom, D.J.; Vallee, B.L. Blochim. Blochys. Acta 1162, 177-1186, 1993 A.Fitle: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmen A;Reference number: S29833; MUID:93192291; PMID:8448182
OY 7 FOOKHIINTPIICNTIMDNNIYIVGGCKRVNTFIISSATTVKAICTGVINMNV 60	A.Scacesson. S.29434 A.Status: preliminary A.Sesidues: 1.1123 48DN> A.Residues: 1.1123 48DN> A.Nore: this commence was submitted to the Drotein Commence Datahase December 1992
QY 61 LSTTRFQLNTCTRISITPRP-CPXSSRTETNYICVKCB-NQY-PVHF 104	ibonuclease 9.7%; Score 119.5; DB 1; Length 123;

9

Gaps

17;

59

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R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
Mol. Bvol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A;Reference number: A00813; MUID:80075014; PMID:513141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 219, 641-646, 1994
A, Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A, Reference number: S41111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINM 58
                                                                                                                                                                                                                                                                                                                                                                   8 FOROHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.Alternate names: RNase 1; RNase A
C.Species: Antilocapra americana (pronghorn)
C.Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C.Accession: A00813
                                                                  #status experimental
                                                                                                                                                                                                                                                                                                7 FQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFLISSATTVKALCTGV-INMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DWSSFONKHIDYPETSASNPNAYCDLMMORR-NLNPTKCKTRNTFVHASPSEIQOVCGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKÝNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-
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C.Skeywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26.84,40-95,58-110,65-72/Disulfide bonds: #status predicted
hydrolase; nucleic acid digestion; pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                        60 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF
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                                                                                                                                                                Length 124;
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                        F:12.41,119/Active site: His, Lys, His #status predicted
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status e:
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                   DB 1;
                                                                                                                                                                Score 132.5; DB 1
Pred. No. 3.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126.5; DB 2
Pred. No. 1.3e-05;
                                                                                                                                                                                                                       19; Mismatches
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R;Zhao, W.; Beintema, J.J.; Hofsteenge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: pancreatic ribonuclease
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                                                                                                                                                            ch 21.9%;
1 Similarity 31.6%;
36; Conservative 1:
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Best Local Similarity 29...
34; Conservative
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A;Molecule type: protein
A;Residues: 1-124 <BEI>
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Matches 36; Conserv
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                 Successions. Stockers (EC 3.1.27.5) BRb precursor, brain - bovine C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Species: Bos primigenius taurus (cattle)
C.Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C.Accession: 820066; JX0006
R.Sasso, M.B.; Carsana, A.; Confallone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A.Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A.Reference number: $20066, MUID:92093604; PMID:1754384
A.Accession: $20066
A.Molecule type: DNA
A.Residues: 1-167 ***CASA>
A.Residues: 17-167 ***C
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pancreatic ribonuclease (EC 3.1.27.5) - pig
NyAlternate names: RNase 1; RNase A
C; Species: Sus scrofa domestica (domestic pig)
C; Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 03-Jun-1994
C; Accession: A92071; A91391; A00816
R; Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A; Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A; Accession: A92071
A; Molecule type: protein
A; Residues: 1, Co', 3-124 < AGC>
R; Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
R; Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Deintema, J.J.
A; Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A; Reference number: A91391
A; Areference number: A91391
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A, Residues: 1-124 < WIES
R; Phelan, V.J.; Hirs, C.H.W.
J. Blod. Chem. 245, 654-661, 1970
A, Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide A, Contents: annotation; disulfide bonds
C, Superfamily: pancreatic ribonuclease
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31.4%; Pred. No. 3.7e-06;
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Matches 38; Conserv
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Gaps

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experimental

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39:

DB 1; Length 124;

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C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
Biochem. J. 157, 317-323, 1976
A;Atitle: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
                                                                                                                                                                                                                                                                A, Molecule type: protein
A, Residues: 1-124 cEMA:
C, Residues: 1-124 cEMA:
C, Superfamily: partenatic ribonuclease
C, Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F12, 44, 119/Active site: His, Lys, His #status predicted
F, 26-84, 40-95, 58-110, 65-72/pisulfide bonds: #status predicted
F, 76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FQQKHII-----NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenin precursor - mouse
NyAlternate names: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 L-----STIRFQLNTCIRISITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LCKNGRINCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 FOROHMDSGNSPGNNPNYCNOMMARR-KMTOGRCKPVNTFVHESLEDVKAVCS---OKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Resides: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RjBond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DN
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.4%; Score 135.5; DB 1
33.3%; Pred. No. 1.7e-06;
iive 16; Mismatches 39
RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: ||| ||||
123 FRHVVIACENGLPVHF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39; Conservative
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Best Local Similarity
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Best Local Similarity
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N;Alternate names:
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R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
D; Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y.; Okazaki, T.; Ohg
                                                                                                                                                                                                                                                                                                                   pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbelana (bullfrog)
C;Species: Rana catesbelana (bullfrog)
C;Species: Rana catesbelana (bullfrog)
C;Daccession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.;
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbelana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Nolecule type: procein
A;Residues: 1-111 < NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutuamic acid
F;10,35,104/Active site: His, Lys, His #status predicted
F;10,35,104/Active site: His, Lys, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NWAIFQOKHIINTPII-CNIIMDNNIYIVGGOCKRVNIFIISSATTVKAICTGVI-NMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
9
                                         2 NWAKFQEKHIPNISNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRNV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribonuclease-related anti-tumor protein - northern leopard frog (fragment) C;Species: Rana pipiens (northern leopard frog) C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
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NWATFOOKHIINTP-IICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INMNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                     61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                              LSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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49.1%; Pred. No. 3.6e-20;
tive 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 60.9%; Score 369; DB 2)
Local Similarity 65.5%; Pred. No. 1e-29;
les 72; Conservative 9; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease
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Best Local Similarity
Matches 54; Conserv
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Best Local S
Matches 72
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NRWHK
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                                                                                                                                                                                                                                                                                                         JX0085
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F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrollidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                  C; Kerwords: anglogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 CKDVNTFTHGNKSNIKAICGANGSPYRENLRMSKSPFÖVTTCKHTGGSPRPFCQYRASAG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 CKRVNTFIISSATTVKAIC---TGVINMAV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%; Score 135.5; DB 1; 39.5%; Pred. No. 2e-06; tive 12; Mismatches 29;
```

RESULT 7

minke whale

pancreatic ribonuclease (EC 3.1.27.5)

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

protein search, using sw model protein ĕ

May 11, 2004, 14:31:13 ; Search time 13.5611 Seconds (without alignments) 787.345 Million cell updates/sec Run on:

US-09-961-400-26

score: Perfect

606 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

DB Minimum I Maximum I

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribonuclease-relat	ribonuclease-relat	pancreatic ribonuc		pancreatic ribonuc	angiogenin precurs	٠.	pancreatic ribonuc		끕		pancreatic ribonuc		pancreatic ribonuc	pancreatic ribonuc	ribonuclease - dom	angiogenin [valida		angiogenin - rabbi	pr		pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc					
SUMMARIES																														
SUMMA	ID	A27121	JX0120	JX0085	A39035	NRWHK	A35932	820066	NRPG	841111	NRPRH	NRKGR	NRCU	NRMS	A43825	NRGPB	NRHO	NRCM	NRCMM	NRCMB	NRKS	S08549	A32474	NRDEN	B43825	NRHUAG	NRGF	NRDEO	S22808	NRBOB
	DB	7	Н	7	~1	Н	Н	C)	Н	~	Н	Н	Н	٦	Н	H	~	гd	٦	Н	Н	7		٦	Н	Н	٦	H	7	Н
	Length	111	111	111	104	124	145	167	124	119	124	122	128	149	123	128	128	124	124	124	128	124	125	124	125	147	124	124	130	124
	% Query Match	96.8	74.3	6.09	45.0	22.4	22.4	22.0	21.9	20.9	20.2	20.1	19.9	19.9	19.7	19.6	19.4	19.2	19.2	19.2	19.2	18.9	18.8	•	æ	•	•	18.6	18.4	18.2
	Score	586.5	450	369	272.5	135.5	135.5	133.5	132.5	126.5	122.5	N		120.5	119.5			116.5	116.5	116.5	116.5	114.5	114	113.5	113.5	113		112.5		110.5
	Result No.	щ	2	3	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

pancreatic ribonuc		pancreatic ribonuc	eosinophil-derived	pancreatic ribonuc	seminal ribonuclea	seminal ribonuclea	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc				
NRWB NREKN	7141	30	1900	3H	0115	en En	ŁT.	ΗĐ	7498	30S	N.S	DEF	1503	3546
NR	30	NR	.9I	NR	Š	NR	NR	NR	A4.	NR	NR	NR	SÓ	SO
Η.	4 (7)	П	7	٦	N	1	Н	Н	4	Н	Н	٦	7	7
124	124	150	158	124	119	124	152	124	125	150	124	124	125	124
18.2	18.2	18.2	18.2	18.1	17.9	17.9	17.9	17.6	17.6	17.6	17.2	17.2	17.2	17.1
110.5	110.5	110.5	110.5	109.5	108.5	108.5	108.5	106.5	106.5	106.5	104.5	104.5	104	103.5
0 -	2 2	33	×	55	9	3.7	88	6	0	급	ď	53	4	ı.

## ALIGNMENTS

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Fibonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi Biochemistry 26, 2189-2194, 1987
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 1-111 c1TT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.8%; Score 586.5; DB 2;
nilarity 99.1%; Pred. No. 2.5e-51;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
Matches 1099
RESULT
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2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61 STIRFQLNICTRISIIPRPCPYSSRIEINVICVKCENQYPVHFAGIGRCP 111 STTREQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111 62 62 Db ò g

RESULT 2

ribonuclease-related sialic acid-binding lectin - Japanese frog C;Species: Rana japonica (Japanese frog) C;Species: Rana japonica (Japanese frog) C;Accession: U-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JX0120 R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990 A;File: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs. A;Reference number: JX0120; MUID:91035319; PMID:2229005

A Molecule type: protein
A; Residues: 1-111 < KGM**
A; Residues: 1-111 < KGM**
A; Experimental source: egg
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Steywords: lectin; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 19-72, 34-82, 52-97, 94-111/Disulfide bonds: #status experimental

Gaps 5, Query Match 74.3%; Score 450; DB 1; Length 111; Best Local Similarity 78.2%; Pred. No. 9e-38; Matches 86; Conservative 7; Mismatches 15; Indels

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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTW) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new thom the compared to none and also the compared to none and also
Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                               Page 75; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        lower immunogenicity in humans
                                 particularly tumour cells.
                                                                                 Disclosure;
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Sequence 355 AA;

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4
                                                                 1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
                           Gaps
                                                                                               NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                             6
  Length 355;
                           Indels
   DB 2;
46.5%; Score 281.5; DB 2
50.0%; Pred. No. 1.3e-23;
cive 15; Mismatches 32
                         Conservative
Query Match
Best Local Similarity
                         26;
                                                                                                 59
                         Matches
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AAW35129 standard; protein; 355 AA (first entry) 20-APR-1998 RESULT 15 AAW35129 

RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog. R. pipiens recombinant RNase rOnc fusion protein 5.

Rana pipiens Synthetic.

WO9731116-A2 28-AUG-1997 97WO-US002588

96US-0011800P. 21-FEB-1996;

Wlodawer A; Boque L, Rybak SM, Newton DL,

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

WPI; 1997-435168/40 N-PSDB; AAT94967

Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. Page 71; 90pp; English. Disclosure;

Ribonuclease molecules based on native Onconase - used for killing cells, particularly tumour cells.

They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans 4 1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58 Gaps 59 NVLSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 110 9 Length 355; 46.5%; Score 281.5; DB 2; Length 50.0%; Pred. No. 1.3e-23; ive 15; Mismatches 32; Indels 56; Conservative Query Match Best Local Similarity Sequence 355 AA; Matches 8X8888888X8 à a  $\delta$ 

Search completed: May 11, 2004, 14:34:32 Job time : 50.7285 secs

SM,

Rybak

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Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (ronc) which are modifications of the RNase Onconase (RTW) (nonc). Such movel ribonuclasse molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also
                                                                                                                                                            Ribonuclease molecules based on native Onconase - used for killing cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.
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nes 32;
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                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%; Score 281.5;
50.0%; Pred. No. 8.8e
cive 15; Mismatches
                                                                       Wlodawer
                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                        Disclosure; Page 77; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW35133 standard; protein; 355 AA.
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                                                                       Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                lower immunogenicity in humans
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96US-0011800P
                                                                                                                                                                                   particularly tumour cells.
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                                                                       Newton DL,
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                                                                                                          WPI; 1997-435168/40.
N-PSDB; AAT94973.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 254 AA;
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Synthetic.
21-FEB-1996;
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                                                                         Rybak SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribonuclease molecules based on native Onconase - used for killing cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 NVLTTSEPYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic; onconase; nonc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R. pipiens recombinant RNase rOnc fusion protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.5%; Score 281.5; DB 2
50.0%; Pred. No. 8.7e-24;
iive 15; Mismatches 32
                                                                                                                                                                                                                                               Wlodawer A;
                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 76; 90pp; English.
                                                                                                                                                                                                                                                 Boque L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US002588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour cell growth; frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNase A; ribonuclease;
                                                                                                                                                                                                                                                 Newton DL,
                                                                                                                                                                                                                                                                                    WPI; 1997-435168/40.
N-PSDB; AAT94972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens.
Synthetic.
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     Rana pipiens.
                                                             WO9731116-A2
                                                                                                                                     19-FEB-1997;
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                                                                                                28-AUG-1997
                           Synthetic.
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Query Match

AAW35135

RESULT 13 AAW35135

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g à

4;

Gaps

6

Length 254; Indels us-09-961-400-26.rag

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v; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; cell growth; frog.

    R. pipiens recombinant RNase protein NLSMetSerrOnc.

                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                20-APR-1998
                                                                                                                                                                   Rana pipiens
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                                                                                                                  RNase A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein with Met at position. Carboxy terminal end of recombinant
RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
antibody directed against CD2 on cancerous B cells or human chorionic
gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
ribonucleases can be expressed in bacteria without an N-terminal
methionine due to the presence of a signal peptide that is cleaved by
bacteria. The soluble expression of ribonuclease allows the proteins to
be fused in-frame with ligand binding moieties to form cytotoxic fusion
proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                              Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; coalently bound; LL2 antibody; ligand binding molety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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49.1%; Pred. No. 2.9e-24;
tive 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                                                      /note= "Met not found in wild type RaPLR1"
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                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                            AAY28867 standard, protein, 105 AA
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                                                                                                                                Recombinant Met(-1) RaPLR1.
                                                                                              (first entry)
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Best Local Similarity
Thes 55; Conserve
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                                                                                                                                                                                                                                    autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                     Rana pipiens
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                                                                                              25-JAN-2000
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                                                                                                                                                                                                                                                                                     Synthetic.
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                                                            AAY28867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
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            4AY28867
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AAW35115 to AAW35123 encode recombinant proteins (ronc) which are modifications of the RNase Onconase (RTM) (nonc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used increased cytotoxic activity compared to nonc and also lower immunogenicity in humans
                                                                                                                                            Ribonuclease molecules based on native Onconase - used for killing cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW35134 standard; protein; 251 AA.
                                                                                                                                                                                                                                Claim 18; Page 63; 90pp; English.
Boque L,
                                                                                                                                                                          particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
  Newton DL,
                                                        WPI; 1997-435168/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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AAW35118 standard; protein; 112 AA

AAW35118 ID AAW3

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Query Match
Best Local Similarity
                 Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9639428-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ardelt WJ;
                                                                                                                                                                                                                                                                                                                                            AAW06544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                 Matches
                                                                                                                                                                                                                                                                                         AAW06544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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So
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                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaplR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                     61
                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
(Rana catesbeiana) lectin used to describe the method of the invention
                                                                                                                                                         2 NWATFQQKHINTPINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                     3 NWATFQQXHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1, CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B ce. Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease; RNase.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g
                                                                                                                                                                                                       STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                     ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                Length 111;
                                                                                                                                                                                                                            STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Met not found in wild type RaPLR1"
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                     Score 586.5; DB 2;
Pred. No. 3.6e-59;
----rhes 0;
                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            AAY28871 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0079751P.
                                                                   96.8%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 34; Page 61; 71pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ08129.
                                     Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07~0CT~1999
                                                                                                     Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
                                                                                                                                                                                                                                                                                                                                                              AAY28871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW6543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
                                                                                                            1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
                                                                                                                                                           1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGILASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                   59 NVLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                    LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
; Score 285.5; DB 2;
; Pred. No. 1e-24;
15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.6%; Score 282.5; DB 2
50.0%; Pred. No. 2.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             AAW06544 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US008304.
     47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00467955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55; Conservative
                                                          56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 104 AA;
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Gaps

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Score 591, DB 2; Length 11 Pred. No. 1.1e-59; 2; Mismatches 0; Indels

97.5%; 98.2%;

62

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3 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                            107; Conservative
         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5955073-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                            Matches
                                                                                                                                                                                                                                    AAY33321
                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribonuclease (RacORI) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RacORI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and
                                                                                          9
                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RaCORI Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarroma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                          1 MQNWATFQQKHINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                            0; Gaps
                                                                                                                                                                           LSTTRFQLNTCTRISITPRPCPYSSRIBINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                        LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is a recombinant Rana catesbelana oocyte
                           Length 111;
                                                                                                                                                                                                                                                                                                                                                              Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Met replaced with Leu"
                                                           1,
                             DB 2;
                Score 596; Db 2,
                                         Pred. No. 3e-6
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                   A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 64; 71pp; English.
                                                                                                                                                                                                                                                                  AAY28874 standard; protein; 110
                             98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079751P
                                                                                                                                                                                                                                                                                                                               (first entry)
                                            Best Local Similarity 97.3
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana catesbeiana
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Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rybak SM,
                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                 AAY28874;
                               Query Match
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marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV) -1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-Anon-B, and delta), herpes zoster, cytomegalovirus)) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells
          61
                                                                                                                                                                                                                                                                                                                                                                  Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain; heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; immune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
2 NWATFQQKHIINTFIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antly fused pancreatic RNase-targeting proteins useful for tumors, infections, immune or autoimmune disorders and as
                                                                              62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                      111
                                                      63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RJ;
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                                                                                                                                                                                                   AAY33321 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 19; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00510696.
91US-00779195.
93US-00014082.
93US-00125462.
                                                                                                                                                                                                                                                                                                                             Frog lectin protein fragment.
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-560488/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1990;
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autoimmune diseases

Sequence 110 AA;

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Gaps

; 0

0; Indels

Mismatches

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109; Conservative
    Matches
                                                                                                                                                             RESULT 5
                                                                                                                                                                            AAY28876
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                                  8
                                                                                       ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Raposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form autoimmune diseases
                                                                                                                                  61
                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana oocyte ribonuclease, RaCORI; covalently bound; CD22; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
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                                                                                                                                                       SIWATFQQKHIINTFIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                  SNWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNUL
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                             Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
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                                                                                                                                                                                                           STIRFQLNICIRISIIPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP
                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant ribonucleases, used for killing target cel
treating cancers, viral infections or autoimmune diseases.
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                                                                          Score 601; DB 2; I
Pred. No. 7.9e-61;
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                                                                                    100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                            AAY28872 standard; protein; 110
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N-PSDB; AAZ08130.
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                                                                                         Local Similarity
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                                                                                                        110;
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98.5%; Score 597; DB 2; Length 110; 100.0%; Pred. No. 2.3e-60;

Best Local Similarity

Query Match

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gonadotrophin (NG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a recombinant Rana catesbelana occyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, Met23Leu and Met5Bleu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding molety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic
                                                                                                                                                                                                                                                                                                                      Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LL2 antibody; ligand binding molety: cancerous B cell; Kaposli's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
62
                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "(His)6 histidine tag attached to N-terminal Met"
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                              NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
NWATFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
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                                                                  111
                                                                                     62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                            Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
                                                                  TTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Met not found in wild type RaCOR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Met replaced with Leu"
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                                                                                                                                                                                         AAY28876 standard; protein; 111
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can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is clavade by bacteria. The soluble expression of fibonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonuclease (RacORI) protein with Met at position I. Carboxy terminal end of recombinant RacORI has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease, RaCOR1, CD22, covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
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                                                                                                                                                                                                                                                                           1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                                                                                                                        DB 2; Length 111;
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                                                                                                                                                                                     100.0%; Score 606; DB 2; 100.0%; Pred. No. 2.1e-61;
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                                                                                                                                                                                                        Best Local Similarity 100.
Matches 111; Conservative
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                                                                                                                       autoimmune diseases
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Best Local Similarity
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                                                                                                                                                     Sequence 111 AA;
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Misc-difference
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                                                                                                                                                                                                                   1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                          1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Rana catesbeiana oocyte ribonuclease; RaCORI Gln1Ser; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclasse allows the proteins to be fused in-frame with ligand binding moleties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
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                                                                                                                                                                                 Gaps
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                                                                                                                                          Score 602; DB 2;
Pred. No. 6.1e-61;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant RaCOR1 Gln1Ser amino acid sequence.
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                                                                       autoimmune diseases
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                                                                                                        Sequence 111 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein May 11, 2004, 14:23:43 ; Search time 50.7285 Seconds (without alignments) 618.248 Million cell updates/sec о По Run

606 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 US-09-961-400-26 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

residues 1586107 seqs, 282547505 Searched:

1586107 hits satisfying chosen parameters: Total number of

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Aay28878 Recombina	Aay28873 Recombina	Aay28877 Recombina	728872 Rana cate		Recon	Aay33321 Frog lect	Aay28871 Recombina	Aaw06544 Antitumou	Aay28867 Recombina	α.	Aaw35134 R. pipien	Aaw35135 R. pipien	Aaw35133 R. pipien	Aaw35129 R. pipien	Aaw35132 R. pipien		Aay28869 Recombina	ĸ	Aay39400 Recombina	垊	Aaw35130 R. pipien	Rana	Aaw35116 R. pipien	Aay28879 Rana pipi	
	Des	Aay	Aay	Aay	Aay28	Aay	Aay	Aay	Aay	Aaw	Aay	Aaw	Aaw	Aaw	Aaw	Aaw	Aaw	Aay	Aay	Aaw	Aay	Aaw	Aaw	Aay	Aan	Aay	
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1		N	AAY28873	AAY28877	AAY28872	AAY28876	AAY28874	AAY33321	AAY2887	AAW06544	AAY28867	AAW35118	AAW35134	AAW35135	AAW3513	AAW35129	AAW35132	AAY28870	AAY28869	AAW35123	AAY39400	AAW35125	AAW35130	AAY28865	AAW35116	AAY2887	
	£	AAY	AAY	AAY	AAY	AAY	AAY	AAY	AAY	AAW	AAY	AAW	AAW	AAW	AAW	AAW	AAW	AAY	AAY	AAM	AAY	AAM	AAN	AAY	AAN	AA	
	DB	73	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~				7						
	Query Match Length	111	111	110	110	111	110	111	105	104	105	112	251	254	355	355	366	104	105	105	105	355	358	104	105	127	
оķо	Query Match	100.0	99.3	99.5	98.5	98.3	97.5	96.8	47.1	46.6	46.5	46.5	46.5	46.5		46.5	46.5	4	4	45.8	45.8	45.8	45.8	45.6	45.6	45.6	
	Score	909	602	601	597	596	591	586.5				281.5					281.5	280.5	278.5	277.5	277.5	77.	277.5	76.	76.	276.5	
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The present sequence is a recombinant Rana catesbelana ribonuclease (RaCCRI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding molety, which

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 68; 71pp; English.

	Aaw00736 Protein d Aaw14065 Onconase Aaw06543 Antitumou	Aaw30301 Recombina Aaw88233 Rana pipi Aay33322 Frog onco	Ami	Aaw35122 R. pipien Aaw35117 R. pipien Aaw35127 R. pipien	Aaw35131 R. pipien Aaw35126 R. pipien	ᅜᄶ	Aab31667 Amino aci Abg31617 Northern
AAY28866 AAR12344 AAR47303	AAW00736 AAW14065 AAW06543	AAW30301 AAW88233 AAY33322	AAB31666 ABG32650	AAW35122 AAW35117 AAW35127	AAW3512/ AAW35131 AAW35126	AAW35115 AAW30302	AAB31667 ABG31617
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104 104 104	101 104 104	104 104	104	106	365	105	104
45.1 45.0 45.0	45.0 45.0 45.0	45.0 45.0	45.0	4.5 6.0 6.0 6.0	45.0	44.6	44.1 44.1
273.5 272.5 272.5	272.5 272.5 272.5	272.5 272.5 272.5	272.5	272.5	272.5	270.5	267.5 267.5
26 27 28	29 30 31	8 8 8 8 8 4	35 36	38	0 4 4 0 1 1	4243	44

### ALIGNMENTS

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Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Glniser; Racori; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; stapei's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease.
                                                                                                                                                                                                                   'note= "Met not found in wild type RaCOR1"
                                                                                                                                                                                                                                         /note= "Wild type Gln replaced with Ser"
                                                                                Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                 Location/Qualifiers
                    Ä.
                    AAY28878 standard; protein; 111
                                                                                                                                                                                                                                                                                                       99WO-US006641.
                                                                                                                                                                                                                                                                                                                          98US-0079751P.
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-610847/52.
N-PSDB; AAZ08135.
                                                                                                                                                                 Rana catesbeiana.
Synthetic.
                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                             WO9950398-A2
                                                                                                                                                                                                                                                                                                                          27-MAR-1998;
                                                             25-JAN-2000
                                                                                                                                                                                                                                                                                   07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                  Rybak SM,
                                        AAY28878;
RESULT 1
           AAY28878
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Sequence 1. Application US/0887811

Pagent No. 6045739

Requence 1. Application US/0887811

Replicable No. 6045739

Replicable New Sequence 1. Application US/0887811

Replicable New Sequence 1. Application US/088781

Replicable New Sequence 1. Distance 1. APPLICANT: New Sequence 1. Distance 1. Dista
```

Search completed: May 11, 2004, 14:37:53 Job time : 16.4253 secs

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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORATION FOR SEG ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 104 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                   San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..104
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-891-848-13
US-08-891-848-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                               GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STREET: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.3%; Score 272.5; DB 1;
49.1%; Pred. No. 3.5e-24;
tive 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
FRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                             STATE: New COUNTRY: USA ZIP: 01078-01883 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: Ploppy disk MEDIUM TYPE: TomeM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5007 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELER No. 5728805 Applicable
INFORMATION FOR SEQ ID No. 1:
SEQUENCE CHARACTERISTICS:
                                        Sequence 1, Application US/08467955
Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 49.19
Matches 54; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-467-955-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH:
                         US-08-467-955-1
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2 NWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV 59 2 DWLTFOKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57 Gaps ., 6 60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109 Length 104; Sequence 13, Application US/08891848

Patent No. 5955073

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: Newton, Dianne L.

APPLICANT: Nicholls, Peter J.

TITLE OF INVENTION: Selective RNase Cytotoxic Reagents

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Two Embarcadero Center, Eighth Floor

STREET: Two Embarcadero Center, Eighth Floor 32; Indels /label= Onc /note= "Onconase from Rana pipiens" COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
COMPOTER: IBW PC compatible
SUCHARE: PETCHTON DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US 08/14,082
FILING DATE: 22-SEP-1993
PRIOR APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
APPLICATION NUMBER: US 07/779,195
FILING DATE: 20-APR-1990
ATTORNEY AGENT INFORMATION:
NAME: Weber, Ellen Lauver:
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
FERENCE/DOCKET NUMBER: 32,762
FERENCE/DOCKET NUMBER: 32,762
FERENCE/DOCKET NUMBER: 32,762 DB 2; Score 272.5; DB 2 Pred. No. 3.5e-24; 15; Mismatches 58 q

58

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Query Match
Best Local Similarity
Matches 54; Conserva
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ZIP: 11202-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: N
FRAGMENT ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE:
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                                                                                                            US-07-921-619-1
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                    1 SNWAŢFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
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                                                                                                                                                                                        Sequence 1, Application US/08283971

Patent No. 5529775

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Mikulski, Stanislaw M.

TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.

STREET: P.O. Box 020083, General Post Office
                                                                                         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠,
د.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 718-625-0399
TELEX: No. 5529775 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                 CITY: Brooklyn STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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HYPOTHETICAL: )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                               US-08-283-971-1
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2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
                                                                                                                                                                      Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 45.3%; Score 272.5; DB 1; Similarity 49.1%; Pred. No. 3.5e-24; 54; Conservative 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NDATA:
APPLICATION NDAER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
RIOR APPLICATION DATA:
APPLICATION NAMER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark E.
REGISTRATION NUMBER: 27507
REGISTRATION NUMBER: 27507
RECISTRATION NUMBER: 2505 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 718-625-0399
TELEFAX: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 718-625-0399
TELEX: No. 559734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 104 amino acids
AMINO ACID
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MEDIUM TYPE: Floppy
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1 SNWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN 58
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                                                                                                                                                                                                    Length 355;
                                                                                                                                                                                                    ch 46.0%; Score 276.5; DB 3; Length 1 Similarity 49.5%; Pred. No. 5.4e-24; 55; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                           ; LOCATION: 1..355
; OTHER INFORMATION: /note= "E6FB[Met-(-1)]SerrOnc"
US-08-875-811-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 015280-244100US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 55, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 amino acids
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Best Local Similarity 49.55
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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                       TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                           Query Match
Best Local Similarity
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STRANDEDNESS:
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US-08-875-811-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SDWLTFQKKAITNTRDVDCDNIMSTNLF----HCKDKNTFIYSREFVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                           Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybac Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Lluis
APPLICANT: WINENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.0%; Score 276.5; DB 3; Best Local Similarity 49.5%; Pred. No. 5.4e-24; Matches 55; Conservative 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STATE: San Francisco STATE: California COUNTRY: USA ZIP: 9411-3834
COUNTRR EADABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                             015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                             NAME: Faris, Susan K.
REGISTRATION UNUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01528
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0200
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                          TYPE: amino acids
TOPOLOGY: lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
    FILING DATE: 21-FEB-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-875-811-64
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, MOLECULE TYPE: protein US-08-875-811-49
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||||:||||| : |: |: || |: |
2 SDWLTFQKKHIINTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
ADDRESSED: Townsend and Townsend and Crew LLP
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILLING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Enharcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.0%; Score 276.5; DB 3 49.5%; Pred. No. 3.6e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 254 amino acids
amino acid
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Matches 55; Conserv
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                                                                                                                                                                                 USA
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1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355;
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 276.5;
Pred. No. 5.4
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 60/011,800
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                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.5
Matches 55; Conservative
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CITY: San Francisco
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셤 δ 임

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148 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
65 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 276.5; DB 3; Length
; Pred. No. 3.5e-24;
15; Mismatches 32; Indels
                                                                                                                                                                                                APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: US/08/875,811
FILLING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                            SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-FEB-1998
CIASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FRID APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FATIS, SUSAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                 ; Sequence 59, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61, Application US/08875811;
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-875-811-59
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                         RESULT 5
US-08-875-811-59
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US-08-875-811-61
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                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
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                                                                                                                                                           2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                       2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                    60 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                            9
                                                                 Length 104;
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                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FBB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                               47.0%; Score 282.5; DB 1; 50.0%; Pred. No. 2.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.0%; Score 276.5; DB 3. Best Local Similarity 49.5%; Pred. No. 1.3e-24; Matches 55; Conservative 15; Mismatches 32.
                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Faris, Susan K.
REGISTRATION INVBEER: 41,739
REFERENCE/DOCKET NUMBER: 0152:
TELEPHONE: (415) 576-0200
INFORMATION: 575-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTER: 22. 2411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~MEDIUM TYPE: IBM PC compatible
~~MEDIUM TYPE: IBM PC compatible
  DEVELOPMENTAL STAGE: Occyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 112 amino acids
amino acid
                                                                                                              55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                 Query Match
Best Local Similarity
Matches 55; Conserv
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US-08-875-811-32
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US-08-467-955-2
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Matches
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Gaps

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ANTI-SENSE: N
FRAGMENT TYPE: N-termina!
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
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TELEX: No
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US-08-467-955-2
                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                          2 NWAIFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNIFIISSATIVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 SITREQLNICTRISITEREDCESSSRIEINVICKKENQYEVHEAGIGRCE 111
                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
COMPTOTE: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
SOCTAME: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFRENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUTICATION INFORMATION:
                                                                                                                                         /note= "Frog Lectin from Rana
catesbeiana"
                                                                                                                                                                                                                                      97.6%; Score 586.5; DB 2;
99.1%; Pred. No. 1.9e-60;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CTTY: San Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.19
Matches 109; Conservative
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FEATURE:
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                                                                                                                     LOCATION: 1..111
CTHER INFORMATION:
CTHER INFORMATION:
US-08-891-848-12
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                                                                                               NAME/KEY: Protein
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2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                                                                                                                                                                               2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGGVINMNVL
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
                                                                                                                                                                    ;;
                                                                                                                                                                                                                                                                                                                                  61 STTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                  62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                          97.6%; Score 586.5; DB 3; Length 111; 99.1%; Pred. No. 1.9e-60; Live 0; Mismatches 0; Indels 1
) OTHER INFORMATION: /note= "Frog Lectin from Rana; OTHER INFORMATION: catesbelana" US-08-875-811-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/436,141
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: A PACHOLIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: No. 5728805 Applicable INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 amino acids
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                                                                                                                                       Best Local Similarity 99.13
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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TELEPHONE:
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US-08-891-848-12
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239.5
231.5
226
272.5
271.5
269.5
269.5
267.5
267.5
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Appli
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Appli
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                                                                                                                                                          (without alignments)
345.738 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-626-429-2
US-09-095-429-2
US-09-394-268-2
US-09-887-748-2
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US-08-875-811-47
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US-08-875-811-20
US-08-875-811-20
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## ALIGNMENTS

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US-08-891-848-12
| Sequence 12, Application US/08891848
| Setent No. 5955073
| GENERAL INCORMATION:
| APPLICANT: Youle, Richard J. APPLICANT: Wishols, Peter J. CANT. Newton, Dianne L. APPLICANT: Newton, Dianne L. APPLICANT: Nichols, Peter J. APPLICANT: Nichols, Peter J. APPLICANT: Wichols, Peter J. APPLICANT: Wichols, Peter J. APPLICANT: Wichols, Peter J. APPLICANT: Uscariate and Townsend and Crew LLP STREE: Townsend and Townsend and Crew LLP STREE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COMPUTER: Rendamble Form.
| ADDRESSER: Townsend and Townsend and Crew LLP STREET: Work Transition of Compatible Computers Rendamble Form.
| STATE: California COMPUTER: Rendamble Form. No. 595073 yet assigned COMPUTER: Rendamble Form. No. 595073 yet assigned CLASSIFICATION NUMBER: US/08/91,848 | FILING DATE: No. 595073 yet assigned CLASSIFICATION NUMBER: US 08/125,462 | FILING DATE: 22-SEP-1991 | FILING DATE: 22-SEP-1991 | FILING DATE: 22-SCT-1991 | FILING DATE: 22-SCT-19
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                                                                                     51; Indels 13; Gaps
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
Iguana iguana (Common iguana).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguanidae; Iguaninae; Iguana.
                                                                                                                                                                                                                                                                               21.0%; Score 126.5; DB 1; Length 119; 29.8%; Pred. No. 8.4e-07; tive 16; Mismatches 51; Indels 13;
                                                                    Zhao W., Beintema J.J., Hofsteenge J.; "The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                  6072FB5B7B15BD5A CRC64;
                                                      TISSUE=Pancreas;
MEDLINE=94139745; PubMed=8307028;
                                                                                                                                                                                                                                                                  13324 MW;
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.8%
Matches 34; Conservative
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                                                                                    ribonuclease.";
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Search completed: May 11, 2004, 14:35:04 Job time: 9.95475 secs

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Beintema J.J.;
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                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                   SEQUENCE OF 31-114 FROM N.A. MEDLINE=93367815; PubMed=8360916; Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P., Carsana A., Palmieri M., Furia A.; "Sequences related to the ox pancreatic ribonuclease coding region in the genomic DNA of mammalian species.";
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
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4 Endonuclease; Glycoprotein.
8 EN SIMILARITY.
9 EN SIMILARITY.
10 BY SIMILARITY.
72 BY SIMILARITY.
62 N-LINKED (GLCNAC. ..) (BY SIMILARITY).
2.9 O-LINKED (BY SIMILARITY).
15592 MW; 73745EFE9079591F CRC64;
                                                                                                                            MEDLINE=96139017; PubMed=8587129; Carsana A., Palmieri M., Confalone E., Belintema J.J., Sasso M.P., Carsana A., Palmieri M., Vento M.T., Furia A.; "Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                              J. Mol. Evol. 37:29-35(1993).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 127.5; DB 1; Length 141; 30.6%; Pred. No. 7.8e-07; tive 17; Mismatches 44; Indels 23.
16-OCT-2001 (Rel. 40, Last annotation update) Ribonuclease, brain (EC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S65126; AAB27931.1; ...
HSSP; P06556; ZRNS.
HIGEPPO; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMARY; SM000927; RNASE PC; 1.
PROSTIE; PS00127; RNASE PANCREATIC; 1.
PROSTIE; PS0127; RNASE PANCREATIC; 1.
ACT_SITE
                                      Giraffa camelopardalis (Giraffe)
                                                                                                                                                                                             J. Mol. Evol. 41:850-858(1995).
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O-LINKED (BY SIMILARITY).
                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Axis.
                                                                                                                                                                                                                                                                                                                                                                      "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212;259-268(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                               MEDLINE-98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E95F3757FFC5B233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INASE PANCREATIC; 1.

Endonuclease; Glycoprotein.

1 BY SIMILARITY.

B4 BY SIMILARITY.

B5 BY SIMILARITY.

B7 SIMILARITY.

B8 SIMILARITY.

B9 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.5; DB 1
Pred. No. 8.4e-07;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%;
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Pfam; PF00074; rnaseA; 1.
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                                                                                                                               (Hog deer)
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(Rel. 28,
(Rel. 41,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=57737;
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01-FEB-1994
28-FEB-2003
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P80287;
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7;

RNBR AXIPR

RESULT 14

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6 FQQKHIINTPI----ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINM 57
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-STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                 MEDLINE=97469980; PubMed=9266695; Strydom D.J., Bond M.D., Vallee B.L.; Man angiogenic protein from bowne serum and milk -- purification and primary structure of angiogenin-2."; Eur. J. Biochem. 247:535-544(1997).
-!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity. Has potent angiogenic activity. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.
-!- TISSUE SPECIFICITY: Serum and milk.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bovinae; NoBT TayTh-eora; Bovoidea; NCBT TayTh-eora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; SECOND 2: ANABOR 2: A. T. PROSITE; 1.
HYDROJASE; NOL127; RNASE PAGONUCLEASE; Angiogenesis;
Protein synthesis inhibitor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.6%; Pred. No. 6.8e-07; ive 19; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                            (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                 123 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 127.5;
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10152; 1AGI.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                      Angiogenin-2 (EC 3.1.27.-).
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                      TISSUE=Milk, and Serum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
58 NVL---
                                                                                                                           01-NOV-1997
                                                                                                                                          01-NOV-1997
                                                                                                                                                          28-FEB-2003
                                                                                                 ANG2 BOVIN
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ACT SITE
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                                                                                    ANG2 BOVIN
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                                                                                                               8 POROHMDPDSSSSNSSNYCMLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKERROHMDSGSSSSGNPNYCNOMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---OK 61
                                                                                    6 FOOKHI-----INTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ATFQOKHI-----INTPLICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINM
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Odocoileinae, Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (BY SIMILARITY)
                                                                                                                                             59 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                                                                      67 NGQİNCYQSNSIMHITDCRQİGSSKYPNCAYKASQEQKHİİVACEGNPPVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Secretory ribonuclease genes and pseudogenes in true ruminants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 128.5; DB 1; Length 151; 29.4%; Pred. No. 6.5e-07;
                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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13804 MW; OAC28CDE14111845 CRC64;
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                           22.0%; Score 132.5; DB 1; 31.6%; Pred. No. 2e-07; iive 19; Mismatches 42;
                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-EB-EB-2003 (Rel. 41, Last annotation update)
Capreolus capreolus (Roe deer).
                                                                                                                                                                                                                                                151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM0092; RNASE PC; 1.
PROSITE; PS00127; RNAŠE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Gly
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPRO1427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
Probom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 O.
16971 MW;
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                                                       Conservative
                                                                                                                                                                                                                                                STANDARD;
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151 AA;
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 124 AA;
                                       Local Similarity
les 36; Conserv
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les 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9858;
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                                                                                                                                                                                                                                                CAPCA
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P79351
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                                                                                                                                       MEDLINE=92093604; PubMed=1754384; Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S., Viola M., Palmieri M., Russo E., Furia A.; "Molecular cloning of the gene encoding the bovine brain ribonuclease and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474 (1991).
                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                     Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96139017; PubMed=8587129; Octofalone B., Beintema J.J., Sasso M.P., Carsana A., Palmieri M., Vento M.T., Furia A.; "Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Evol. 41:850-858(1995)...
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133.5; DB 1; Length 167; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                 Ohgi K., Irie M.; "Primary structure of a ribonuclease from bovine brain."; J. Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
Prodom, PD000535; RNASe Pc; 1.
PROSITE; PS00127; RNASE PA: 1.
PROSITE; PS00127; RNASE PA: 1.
PROSITE; PS00127; RNASE PA: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONUCLEASE, BRAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARACTER (GLCNAC. . .).
/FILGE-CAR_000055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> S (IN REF. 2).
681CAAC3CC2FC459 CRC64;
                                                                                                                                                                                                                                          SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (EC 3.1.27.-) (BRB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O-LINKED
                                                                                                                                                                                                                                                                     MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18450 MW;
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31.4%;
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-167 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S81744; AAB36138.1
PIR; S20066; S20066.
HSSP; P00656; 2RNS.
GlycoSuiteDB; P39873; -.
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155
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167
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67
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110
121
136
98
                                                                                    Bovidae; Bovinae; Bos.
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159
155
167 AA;
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Best Local Similarity
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                         TISSUE=Brain;
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                                                                                    58 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
                                                                                                      88 NITCKNGHPNCYQSKSTMSIIDCREIGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147
                           4 ATFOOKHI-----INTPLICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINM 57
                                              Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.; "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence.";
Gaps
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                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 245:654-661(1970).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphotal sand 3'-phosphotaligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653 (1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=70104198; PubMed=4904878;
Phelan J.J., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. 3.
disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; A92071; NRPG.
                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
43; Indels
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BY SIMILARITY.
BY SIMILARITY.
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Mismatches
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCKEAT
Hydrolase; Nuclease; Endonucleas
17;
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InterPro; IPR001427; RNaseA.
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 Conservative
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and mouse cDNA sequences.";
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R. Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

By pleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Porbhywki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Makan J.W., Green E.D., Dickson M.C.,

Rhiting M., Makan J.W., Schmutz J., Myers R.M.,

Rhiting M., Schein J.E., Jones S.J.M., Marra M.A.;

Rhiterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rhiterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rhiterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodeneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last amnotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 124;
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Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.5%; Score 135.5; DB 1;
33.3%; Pred. No. 9.4e-08;
ive 16; Mismatches 39;
                                                                                                                                                                                                                                                               Glycoprotein.
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PRINTS; PR00794; RIBONUCIEASE.
PPTDOON; PD000535; RNASCA, 1.
SMART; SM00092; RNASCA, 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycopx
10 ISULFID 26 84
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                                                            InterPro; IPR001427; RNaseA.
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nes 39; Conservative
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                                    HSSP; P00656; 1SRN
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                   angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically bydrolyzing cellular tRNAs.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1162:177-186(1993).
-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
to actin on the surface of endothelial cells; once bound,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                               MEDLINE-93192291; PubMed-8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
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SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Biochem. J. 157:317-323(1976).
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123 FRYIIGCENGWPVHF 138
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HSSP: P03950: 1A4Y.
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MEDLINE=96079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse anglogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";
Genomics 29:200-206(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
                                           Cell. Biol. 17:1503-1512(1997).
FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PYRROLIDONE CARBOXYLIC ACID
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developmentally regulated genes when expressed in NIH 3T3
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12; Mismatches 23; Indels
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InterPro; IPR00142,, ...
PEAM, PR0074; rnaseA; 1.
R PRODOM; PD000535; RNaseA; 1.
R PROGUE; PS00127; RNASE PC; 1.
R RYART; SW00127; RNASE PC; 1.
R RYGITE; PS00127; RNASE PC; 1.
R HYdrolase; Nuclease; Endomuclease; Angiogenesis; M Hydrolase; Nuclease; Endomuclease; Angiogenesis; M Hydrolase; Inhibitor; Signal; Pyrrolidone can provide and programment of the potential principle of the provided provided programment of the potential principle of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of the programment of 
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Angiogenin-related protein precursor.
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121 KDFRYIVIACEDGWPVHF 138
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InterPro; IPR001427; RNaseA.
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                             fibroblasts."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              064438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGR MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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RRITER SOLUTION SELECTION SOLUTION SELECTION SOLUTION SELECTION SOLUTION SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNIRISKSRRQVTTCTHKGRSPRPPCRYRASKG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITPR-PCPYSSRTE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emmens M., Welling G.W., Beintema J.J.;
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00573; 124 AA.
P00573; 124.1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
RNASEI OR RNSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Balaenoptera acutorostrata (Minke whale) (Lesser rorqual)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.9%; Score 149.5; DB 1
43.4%; Pred. No. 3.5e-09;
iive 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                       MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
Fram; PR00074; rnaseA; 1.
PRINTS; PR00079; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PO.
SPROSTIF; PS00127; RNASE PANCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
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45.3%;
                                                                                                                                       Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 49.1
nes 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                          10
97
97
90
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30
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                                                                                                                                                                                                                                                                                                                                                                                                             104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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97
19
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANG3 MOUSE
P97802;
                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                   ACT SITE
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HEREN COCCOCC
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                                                                                                                                                                                                                                                                                                  2 NWATFOOKHIINTPII-CHTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                  2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens occytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosimann S.C., Ardelt W., James M.N.G.; "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity."; J. Mol. Biol. 236:1141-1153(1994).
          - CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphacligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

- SUBCELLULAR LOCATION: Secreted.

- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ardelt W., Mikulski S.M., Shogen K.; Ardelt W.; Ardino edid sequence of an anti-tumor protein from Rana pipiens cocytes and early embryos. Homology to pancreatic ribonucleases."; J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
2-FBB-2003 (Rel. 41, Last annotation update)
P-30 protein (BC 3.1.27.-) (Onconase).
Rana pipiens (Northern leopard frog).
Rana pipiens (Northern leopard frog).
Amphibia; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NGBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                          62 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93066156; PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                                                                                                                              LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                2
                                                                                                                                       Hydrolase, Nuclease, Endonuclease, Pyrrolidone carboxylic acid. MOD RES
                                                                                                                                                                                                                                                          Length 111;
                                                                                                                                                                                                                                                                               27; Indels
                                                                                                                                                                                                                                       D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                           Score 369; DB 1;
Pred. No. 6.4e-33;
                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PY SIMILARITY.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                        104 AA
                                                                                                                                                                                                                                                                                9; Mismatches
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MEDLINE=94166079; PubMed=8120892;
                                                                                                                               PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91093131; PubMed=1985896;
                                                         PIR, JX0085, JX0085.

PIR, JX0085, JX0085.

HSSP, P11916, 1BG4.

InterPro; IPR001427; RNaseA.

Pfan; PF00074; rnaseA; 1.

ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                      12461 MW;
  Biochem. 106:729-735(1989)
                                                                                                                                                                                                                                                           61.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins 14:392-400(1992).
                                                                                                                      ; SM00092; RNASE_P!
TE; PS00127; RNASE_P!
                                                                                                                                                                                                                                                                     Local Similarity 65.5
les 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                               10
35
104
72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               James M.N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                       RN30 RANPI
P22069;
                                                                                                                                                    MOD RES
ACT_SITE
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ACT_SITE
DISULFID
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                                                                                                                                                                                                                  DISULFID
                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                               RN30 RANPI
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2 NWAIFQOKHIINI-PIICNIIMDNNIYIVGGQCKRVNIFIISSAITVKAICTGVI-NMNV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
                                                                                                           -!- DEVELOPMENTAL STRAGE: Barly embryos (up to four blastomere stage).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; 10NC; 31-3M*-94.

InterPro; 1PR001427; RNaseA.
PEAM; PR00074; MaseA; 1.

ProDom; PD000535; RNaseA; 1.

SWART; SM00092; RNASE PANCREATIC; 1.

Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin-3 precursor (EC 3.1.27.-) (Anglogenin-related protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fu X., Kamps M.P.; "E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11845 MW; 22A753C2F9E566B4 CRC64;
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;; Pred. No. 1.4e
15; Mismatches
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MEDLINE=97184476; PubMed=9032278;
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                           PDB; 1BC4; 28-OCT-98.
PDB; 1BC4; 28-OCT-98.
PDB; 1BC4; 28-OCT-98.
PDB; 1BC4; 28-OCT-98.

InterPro; 1PR001427; RNaseA.
Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNase Pc; 1.
PROSITE; PS00127; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SMART; SM0127; RNASE Paid acid; Lectin; 3D-structure; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1.
22.
CHAIN 23 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STTRFQLNICTRISITPRPCPYSSRIBINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.6%; Score 586.5; DB 1; Length 133; 99.1%; Pred. No. 3.1e-56; tive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                            RIBONUCLEASE, OCCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14762 MW; A7D62594F7D16F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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63
74
74
84
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133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                             23
23
32
57
57
                                                              SUBUNIT:
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ID LECS RANJA
AC P18839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
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ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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SEQUENCE
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Best Local {
                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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(Rel. 16, Created)
(Rel. 28, Last sequence update)
(Rel. 42, Last annotation update)

01-FEB-1990 10-OCT-2003

111 AA

PRT;

STANDARD;

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2 NWAIFQORHIINIP-IICNTIMDNNIYIVGGQCKRVNTFIISSATIVKAICTGV-INMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NWAKFQEKHIPNTSNINCNTIMDKSIYIVGGCKERNTFIISSATTVKAICSGASTNRNV 61
                                                                                                                                                                                                                                                                FUNCTION: The S-lecting in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes. SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Liver;
MEDLINE=9013074; PubMed=2613682;
MEDLINE=90130374; PubMed=2613682;
Mitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Okazaki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                              TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.;
"Akayanagi Y., Titani K.;
"Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Sialic acid-binding lectin (EC 3.1.27.-).
Rama japonica (Japanese reddish frog).
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordaťa; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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                                                                                                                                                                                                                                                                                                                                                           - SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
Prodom; PD000555; RNaseA; 1.
SMART; SM00092; RNASE PO; 1.
PROSITE; PS00127; RNASE PANCEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 450; DB 1;
Pred. No. 1.2e-41;
7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribonuclease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY
BY
BY
                                                                                                                  SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                   J. Biochem. 108:139-143(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
72
82
97
                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JX0120; JX0120.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
52
94
111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                             NCBI TaxID=8402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8400;
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SEQUENCE
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5

us-09-961-400-24.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein May 11, 2004, 14:24:28 ; Search time 9.95475 Seconds (without alignments) 575.375 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-961-400-24 601 1. SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rana	rana	rana	rana	mus		bala	0 mus musculu	pos		l capreolus c						_		_	8 antilocapra	6 macropus ru	6 myocastor c		_	-		-		_	_	_		3 macaca mula
	escr	P11916	P18839	P14626	P22069	P97802	Q64438	1900d	P21570	P39873	P00671	P79351	P80929	029542	P87350	P80287	Q8wn66	Q8wn65	08wn60	Q29543	P00668	P00686	P00676	Q8wn67	P00683	Q8wn61	P31346	P00679	Q8wn62	P00674	P00670	P04059	P15467	Q8wn63
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SUMMARIES		RANCA	RANJA	RANCA	RANPI	<b>JOUSE</b>	YOUSE	ALAC	YOUSE	SOVIN	D.	CAPCA	SOVIN	SIRCA	AXIPR	SUIG	CERAE	MIOIA	SAISC	SHEEP	ANTAM	ACRU	YOCO	PONPY	MOUSE	AOTTR	PIG	CAVPO	SAGOE	HORSE	CAMDR	PROGU	BOVIN	MACMU
SU	Π	RNPO I	LECS	RNPL	RN30	ANG3 MOUSE	ANGR MOUSE	RNP BALAC	ANGI MOUSE	RNBR_BOVIN	RNP PIG	RNBE	ANG2_BOVIN	RNBR GIRCA	RNBR AXIPR	RNP IGUIG	ANGI CERAE		ANGI	RNBR SHEEP	RNP A	RNP MACRU	RNP	ANGI	RNP M	ANGI	ANGI	RNPB	ANGI SAGOE	RNP H	RNP C		RNS4	ANGI MACMU
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	% Query Match Length	133	111	111	104	145	145	124	145	167	124	151	123	141	151	119	146	146	146	143	124	122	128	147	149	146	123	128	146	128	124	128	119	146
	% Query Match	97.6	74.9	61.4	45.3	25.7	24.9			22.2	22.0	21.4	21.2	21.2	21.2	21.0	21.0	21.0	20.8	20.5	20.4	20.3	20.0	0	20.0	20.0	19.9	19.7	19.6	19.6	19.4	19.4	19.2	19.2
	Score	586.5		369	272.5	154.5	149.5	135.5	135.5	133.5	132.5	128.5	127.5	127.5	127.5	126.5	126.5	126.5	125	123.5	122.5	122	120.5	120.5	120.5	120	119.5	118.5	118	117.5	116.5	116.5		115.5
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P10152 bos taurus P00666 rangifer ta P31347 oryctolagus QWwn64 papio hamad P033950 homo sapien	Common pair Lighton P00664 capreolus C P00662 giraffa cam Q91jhi mus musculu P24717 cricetulus O55004 rattus norv Q9wtt5 acomys cahi
ANGI BOVIN RNP RANTA ANGI RABIT ANGI PAPHA ANGI HUMAN	AND TAPE RNP GAPCA RNP GIRCA RNP GRILO RNP GRILO RNS RAT RNP ACOCA
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148 124 146 146	1247 1248 1248 130 147
0.684 0.884 0.686 0.886 0.886 0.886	18.8 18.7 18.7 18.6 18.6 18.6
113.5 113.5 113.5 113.5	113 112.5 112.5 112.5 111.5 111.5
4 72 9 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	6 4 4 4 4 4 6 0 1 2 6 4 6

# ALIGNMENTS

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puncreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
NyAlternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Bergy, A;, van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Bur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Recession: A00826
A;Accession: A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 L-----STIRFQLNTCTRISITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCKNGQINCYQSYSRMRIIDCRVİSSSKFPNCSYRMSQAQKSİIVACEGDPYVPVHF 120
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Best Local Similarity 31.6%; Pred. No. 8.6e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23
                                                                                                                                                                                                                      88 INYICVKCENOYPVHF 103
                                                                                                                                                                                                                                                                                                                       99 FRTIAVACENGLPVHF 114
                     33
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completed: May 11, 2004, 14:37:08 ne : 14.4389 secs

Search cor Job time mouse

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Affacesion: A34090
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Affacesion: A34090
Affacesion: Breliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
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A, Molecule type: MRNA
A, Molecule type: MRNA
A, Molecule type: MID: 92107684; PMID: 1840677
A, Status: preliminary
                                                                                            N; Alternate names: RNase 1; RNase A.
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A34090; S22599; A00830
R;Schueller, C; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of A;Reference number: A34090; MUID:90136034; PMID:2299980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenin - pig
Cispecias: Sus scrofa domestica (domestic pig)
Cispecias: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: S29834; A43825
Ribond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins:
A;Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 FQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 TCKNRKSNCYKSSSALHIIDČHLKGNSKYPNĆDÝKTTQYQKHÍIVAČEGNPÝVPVHF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---STTRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: EMBL:X60103; NID:953981; PIDN:CAA42697.1; PID:953982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Residues: 26-149 clear.
(Superfamily: pancreatic ribonuclease
(S.Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
(S.Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
(F.12-25/Domain: signal sequence #status predicted <SIG>-
(F.14-149)Product: pancreatic ribonuclease #status experimental <WAT>-
(F.27, 66, 144/Active site: His, Lys, His #status predicted
(F.51-109, 65-120, 83-135, 90-97/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: this sequence was submitted to the Protein Sequence Database, C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lenstra, J.A.; Beintema, J.J.
B. Sabochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 120.5; DB 1; Length 130.8%; Pred. No. 6.4e-05; ive 16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ches 35;
                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.9%; Score 119.5;
Best Local Similarity 39.5%; Pred. No. 6.6e
Matches 30; Conservative 6; Mismatches
                                                                      pancreatic ribonuclease (EC 3.1.27.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similaricy
hes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 1-123 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA A; Residues: 1-149 <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 L----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A00830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S29834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
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R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FQRQHMDTEHSTASSSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65
      19
                                                            STTRFQLNTCTRISITPRP-CPYSSRTEINYICVKCE-NQY-PVHF 103
                                                                                                                   62 NVACKNGQINCYQSYSIMSIIDCREIGSSKXPNCAYKIIQAKKHIIVACEGNPYVPVHY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                               MyAlternate names: RNase 1; RNase A
NyAlternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
R;Gasstra, W.; Weilling, G.W.; Beintema, J.J.
Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N, Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NOY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LCKNGQINCYQSNSNMHIIDCRVISNSDYPNCSYRISQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FERQHIDSRGSPSTNPNYCNEMMKSR-NWTQGRCKPVNTFVHEPLADVQAVC---FQKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 1-128 < VAN>
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; R; A1,119,6ctive site: His, Lys, His #status predicted
F; R; A4,10-95,58-110,65-72/Disulfide bonds: #status predicted
F; R; A4,81nding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;11,40,117/Active site: His, Lys, His #status predicted F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 IGVINMAVLSTIRFOLNICIRISIIPRP-CPYSSRIEINYICVKCENQY-PVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 FQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 122; DB 1; ilarity 30.7%; Pred. No. 3.7e-05; Conservative 16; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.0%; Score 120.5; DB 1
31.6%; Pred. No. 5.4e-05;
tive 15; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 1-122 <GAA>
C; Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Pest Local Similarity 31.67
77: Conservative
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Best Local Similarity
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                                                      58 NVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A00833
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7;

Gaps

discernmer

December 1992

#status experimental

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---ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
glycoprotein; hydrolase; nucleic acid digestion; pancreas
                            F.12.41,119/Active site: His, Lys, His #status predicted
F.21,34,76/Binding site: carbohydrate (Asn) (covalent) #status e2
F.26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
                                                                                                                                                         Score 132.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
A, Molecule type: protein
Mesidues: 1-119 < ZHA>
C, Superfamily: pancreatic ribonuclease
                                                                                                                                                         22.0%;
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nes 36; Conserv
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Best Local Similarity
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                         Dancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine C; Species: Bos primigenius taurus (cattle)
C; Apecies: Bos primigenius taurus (cattle)
C; Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C; Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C; Dacession: $20066; JX0056
R; Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res: 19, 6469-6474, 1991
A; Title: Molecular choning of the gene encoding the bovine brain ribonuclease and its ship Reference number: $20066; MUID:92093604; PMID:1754384
A; Accession: $20066
A; Molecule type: DNA
A; Residues: 1-167 CsAA.>
A; Cross-references: EMBL:X59767; NID:9150; PIDN:CAA42439.1; PID:9151
B; Matanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Irii
B; Matanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Irii
B; Matanabe, H.; Katoh, H.; Ishii, M.; Monole Erome brain.
A; Residues: 12-14, S', 156-166 cNAT>
A; Residues: 27-124, S', 156-166 cNAT>
A; Residues: 27-124, S', 156-166 cNAT>
A; Residues: 27-124, S', 156-166 cNAT>
A; Residues: 27-124, S', 159-180; A; Molecule Type succession: Jay. His #status predicted
F; S6-110, 66-121, 44-156, 91-98(Pisulfide bonds: #status experimental
F; 155-110, 66-121, 44-156, 91-98(Pisulfide bonds: #status experimental
F; 155-18niding site: carbohydrate (Rn) (covalent) #status experimental
F; 159/Binding site: carbohydrate (Ser) (covalent) #status experimental
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A; Residues: 1-124 <NIE>
B; Phelan J. J.; Hirs, C.H.W.
B; Phelan J. J.; Hirs, C.H.W.
A; Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bc
A; Reference number: A92072; MUID:70104198; PMID:4904878
A; Contents: annotation; disulfide bonds
C; Superfamily: pancreatic ribonuclease
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A,Molecule type: protein
A,Residues: 1,'Q',3-124 <JAC>
A,Residues: 1,'Q',3-124 <JAC>
R,Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A,Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II. The amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NyAlternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Dacte: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Blol. Cham: 245, 637-653, 1970
A;Till: The primary structure of porcine pancreatic ribonuclease. II. The a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.2%; Score 133.5; DB 2
Best Local Similarity 31.4%; Pred. No. 3.6e-06;
Matches 38; Conservative 17; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) - pig
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pancreatic ribonuclease - common iguana)
C;Species: Iguana iguana (common iguana)
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bicchem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ;
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                                                                     6 FQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGV-INMN 58
                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|::|| || || : :| : :| || || || DWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 NWATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Gaps
                                      Gaps
                                                                                                                                                                    67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVVHF 120
                                                                                                                                                59 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 -TGVINMNVLSTTREQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF
                                  17;
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Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.4%; Score 122.5; DB 1; Length 1
30.3%; Pred. No. 3.3e-05;
ive 18; Mismatches 42; Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
 DB 1;
                 1 Similarity 31.6%; Pred. No. 3.4e-06; 36; Conservative 19; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.0%; Score 126.5; DB 2 29.8%; Pred. No. 1.3e-05;
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ribonuclease.

experimental

23;

DB 1; Length 124;

63

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A; Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues C; Superfamily: pancreatic ribonuclease C; Keywords: anglogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribors
A;Reference number: A00818; WUID: 76277855; PMID: 962870
A;Reference number: A00818; WUID: 76277855; PMID: 962870
A;Residues: 1-124 <a href="https://documber: bordering">https://documber: bordering</a>
A;Residues: 1-124 <a href="https://documber: bordering">https://documber: bordering</a>
C;Reywords: glycoproteain; hydrolase; nucleic acid digestion; pancreas
C;Reywords: glycoproteain; hydrolase; mucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (BC 3.1.27.-)
C;Species: Mus unuclus (house mouse)
C;Species: Mus unuclus (house mouse)
C;Species: Msequence_revision 09-Nov-1990 #text_change 18-Jun-1999
R;Bond, M.D.; Vallee, B.L...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 L-----STIRFQLNTCIRISITPRP-CPYSSRIBINYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 LCKNGRINCYESNSIMHITDCRQ1GSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.5%; Score 135.5; DB 1; Length 145; 39.5%; Pred. No. 2e-06; cive 12; Mismatches 29; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.5%; Score 135.5; DB 1; Length 33.3%; Pred. No. 1.7e-06; ive 16; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F)1-24/Domain: signal sequence #status predicted <SIG>
F)25-145/Product: angiogenin #status predicted <MAT>
F)25/Modified site: pyrrolldone carboxylic acid (Gln) (in F)37,64,137/Acture site: His, Lys, His #status predicted F)50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A; Title: Isolation and sequencing of mouse angiogenin DN
A; Reference number: A35932; MUID:91025023; PMID:2222458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 TNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 FRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.55
Best Local Similarity 33.33
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 39.59
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-145 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A35932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           H.; Abe, Y.; Okazaki, T.; Ohg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
B;Ardelt, W.; Mikulski, S.M.; Shogen, K.
A;Title: Anino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0088
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.;
J. Biochem. 106, 729-735, 1989
A;Title: Pximary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
         59
                                     2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
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   NWATFOOKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DWITFOKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglucamic acid
F:J/Modiled site: pyrrolidone carboxylic acid (Gln) #status experimental
F:J0,35,104/Active site: His, Lys, His #status predicted
F:J9-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                        60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 369; DB 2;
Pred. No. 9.6e-30;
9; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                  pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.4%;
65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.57
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-104 < ARD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-111 <NIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A39035
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mature form) #status predicted

2,

7 RESULT

minke whale

pancreatic ribonuclease (EC 3.1.27.5)

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GenCore version 5.1.6
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- protein search, using sw model OM protein

Run on:

May 11, 2004, 14:31:13 ; Search time 13.4389 Seconds (without alignments) 787.345 Million cell updates/sec

US-09-961-400-24 601

1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	ribonuclease-relat	ribonuclease-relat	pancreatic ribonuc	ribonuclease-relat	pancreatic ribonuc	angiogenin precurs	pancreatic-type ri	pancreatic ribonuc		•										pancreatic ribonuc	ribonuclease - dom			angiogenin - rabbi					
	ID	A27121	JX0120	JX0085	A39035	NRWHK	A35932	S20066	NRPG	841111	NRPRH	NRKGR	NRCU	NRMS	A43825	NRGPB	NRHO	NRCM	NRCMM	NRCMB	NRKS	508549	A32474	NRDEN	B43825	NRHUAG	NRGF	NRDEO	S22808	
	DB	10	7	2	7	Н	Н	7	Н	~	Н	ч	П	Н	Н	Н	Н	Н	Н	Н	Н	7	Н	Н	Н	٦	٦	Н	7	,
	° Query Match Length	111	111	111	104	124	145	167	124	119	124	122	128	149	123	128	128	124	124	124	128	124	125	124	125	147	124	124	130	
ok	Query Match ]	97.6	74.9	61.4	45.3	22.5	22.5	22.2	22.0	21.0	20.4	20.3	20.0	20.0	19.9	19.7	19.6	19.4	19.4	19.4	19.4	19.1	19.0	18.9	18.9	18.8	18.7	18.7	18.6	
	Score	586.5	450	369	272.5	135.5	135.5	133.5	132.5	126.5	122.5	122	120.5	120.5	119.5	118.5	117.5	116.5	116.5	116.5	116.5	114.5	114	113.5	113.5	113	112.5		111.5	
	Result No.	1	8	m	4	D.	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

н	ы	pancreatic ribonuc	pancreatic ribonuc	eosinophil-derived			pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	seminal ribonuclea	seminal ribonuclea	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc
NRWB	NREKN	S07141	NRBO	161900	NRSH	JX0115	NRCB	NRRT	NRHP	A47498	NRBOS	NRGN	NRDEF	S04503	S08546
ત	Н	7	ч	7	Н	7	Н	Н	Н	4	Н	Н	Н	~	7
124	124	124	150	158	124	119	124	152	124	125	150	124	124	125	124
18.4	18.4	18.4	18.4	18.4	18.2	18.1	18.1	18.1	17.7	17.7	17.7	17.4	17.4	17.3	17.2
110.5	110.5	110.5	110.5	110.5	109.5	108.5	108.5	108.5	106.5	106.5	106.5	104.5	104.5	104	103.5
0	-	2	· en	4	2	9	7	œ	o	0		~	٣	4	Ŋ

# ALIGNMENTS

œ	RESULT 1.
ď	A27121
×	ribonuclease-related sialic acid-binding lectin - bullfrog
O	C;Species: Rana catesbeiana (bullfrog)
J	C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
J	C,Accession: A27121
rx.	R,Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi
ш	Biochemistry 26, 2189-2194, 1987
Æ	A, Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbelana)
ra;	A; Reference number: A27121; MUID:87299649; PMID:3304421
ĸ.	A;Accession: A27121
ra;	A;Molecule type: protein
E.	ArResidues: 1-111 <tit></tit>
J	C; Superfamily: pancreatic ribonuclease
J	C; Keywords: lectin
	Query Match 97.6%; Score 586.5; DB 2; Length 111;
	Best Local Similarity 99.1%; Pred. No. 2.3e-51; Matches 109: Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Ū	Qy 2 NWATEQOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIİSSATTVKALCTGVINMNVL 60
•	
-	UD Z NWAIFQKNAINLEINCNIIMDNNIILVOGGCKNANIELLUGGELVGGLGGGGGGGGGGGGGGGGGGGGGGGGGGGG
•	Qy 61 SITRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Н	Db 62 STTRFQLATCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

# RESULT 2 JX0120

ubonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Species: Rana japonica (Japanese frog)
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999
C;Date: Date: procein
A;Reference number: UX0120; MUID:91035319; PMID:2229005
A;Reference number: UX0120; MUID:91035319; PMID:2229005
A;Reference number: Drocein
A;Reference number: Drocein
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A;Reference number: Dr

2; Gaps 2; Query Match

74.9%; Score 450; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 8.6e-38;
Matches 86; Conservative 7; Mismatches 15; Indels

99WO-US006641 98US-0079751P

26-MAR-1999;

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The present sequence is a Rana pipiens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Onconse (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human charionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonucleases allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                    New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 69; 71pp; English
                                                                                                                                                                                  Rybak SM, Newton DL;
                                                                                                                                                                                                                           WPI; 1999-610847/52.
                                                                                                                                                                                                                                              N-PSDB; AAZ08136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases
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2 NWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMAV 59 80 Gaps 9; LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109 Length 127; Indels 46.0%; Score 276.5; DB 2; 49.1%; Pred. No. 1.4e-23; 15; Mismatches Conservative Local Similarity 54; 9 Query Match 원 à ð

AAW35134 standard; protein; 251 AA (first entry) Rana pipiens 20-APR-1998 AAW35134; RESULT 15 

RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog. R. pipiens recombinant RNase ronc fusion protein 10.

WO9731116-A2 28-AUG-1997 97WO-US002588 96US-0011800P. 19-FEB-1997; 21-FEB-1996; (USSH ) US DEPT HEALTH & HUMAN SERVICES

Sequences AAW35125 to AAW35135 represent recombinant fusion proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower immunogenicity in humans Ribonuclease molecules based on native Onconase - used for killing cells, Wlodawer A; Disclosure; Page 76; 90pp; English Boque L, particularly tumour cells. Newton DL, WPI; 1997-435168/40. N-PSDB; AAT94972 Sequence 251 AA; Rybak SM, NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR

1 SNWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN 58 9; Gaps 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109 Length 251; 46.0%; Score 276.5; DB 2; Length 49.5%; Pred. No. 3.38-23; ive 15; Mismatches 32; Indels 55; Conservative Best Local Similarity Query Match Matches ₹ g à

completed: May 11, 2004, 14:34:32 : 51.2715 secs Job time Search

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Wlodawer

Boque L,

97WO-US002588 96US-0011800P

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Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                      Claim 18; Page 63; 90pp; English
                                                                                                                                                                              particularly tumour cells.
                                                                                                           Newton DL,
                                                                                                                                 WPI; 1997-435168/40.
                                                                                                                                            N-PSDB; AAT94955
                                    19-FEB-1997;
                                                            21-FEB-1996;
              28-AUG-1997.
                                                                                                           Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
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                                                                                                                                                                                                                                                                                                                                                        The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NWAIFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                  New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTTREQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 276.5; DB 2; Length 105; 49.1%; Pred. No. 1.1e-23; Live 15; Mismatches 32; Indels 9
                                                                                                 /note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R. pipiens recombinant RNase protein NLSMetSerrOnc.
                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       Claim 34; Page 57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW35118 standard; protein; 112
                                                                                                                                                                    99WO-US006641
                                                                                                                                                                                           98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell growth; frog
                                                                                                                                                                                                                                            Newton DL;
                                                                                                                                                                                                                                                                  WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                              N-PSDB; AAZ08126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 105 AA;
                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9731116-A2
                                       Rana pipiens
                                                                                                                        WO9950398-A2
                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                              27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1998
                                                                                                                                                07-0CT-1999
                                                    Synthetic
                                                                                                                                                                                                                                             Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNase A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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4;
AAW35115 to AAW35123 encode recombinant proteins (ronc) which are modifications of the RNase Onconase (RTM) (nonc). Such novel ribonuclease enclosules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing timeuro cell growth. They can also be used for eell separation in vitro by selectively killing unwanted types of cells, e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to nonc and also lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||||:|||| | : |: || |::
|SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                             SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Rana pipiens_Clone_5alb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                46.0%; Score 276.5; DB 2; 49.5%; Pred. No. 1.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .23
/label= Signal_peptide
/note= "Putative"
24. .127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY28879 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  55; Conservative
                                                                                                                                                                                                                                                             immunogenicity in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9950398-A2
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Rana pipiens liver ribonuclease (RaPLR1).

(first entry)

25-JAN-2000

AAY28865;

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Raposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoximmune disease; RNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SNWATPQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type Gln replaced with Ser"
                                                                                                    Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%; Score 280.5; DB 2; 49.5%; Pred. No. 3.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
AAY28865
ID AAY28865 standard; protein; 104 AA.
 AAY28871 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 34; Page 61; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US006641,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%;
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rybak SM, Newton DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-610847/52.
N-PSDB; AAZ08129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105 AA;
                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                              Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                WO9950398-A2
                                                                    25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                   07-0CT-1999
                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
g
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The present sequence is Rana pipiens liver ribonuclease (RaPLRI) protein. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Met(-1) Rana pipiens ribonuclease, RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
                                                                                                           Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcona; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cyrotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LSTIRFOLNICIRISITPRPCPYSSRIETNYICVKCENOYPVHFAGIGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.0%; Score 276.5; DB 2;
49.1%; Pred. No. 1.1e-23;
cive 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28867 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 55; 71pp; English
                                                                                                                                                                                                                                                                                               99WO-US006641.
                                                                                                                                                                                                                                                                                                                                98US-007975IP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Met(-1) RaPLR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104 AA;
                                                                                                                                                                                                 Rana pipiens
                                                                                                                                                                                                                                 W09950398-A2
                                                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                27-MAR-1998;
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                                                                                                                                                                                                                                                                 07-OCT-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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28

Gaps

6

Indels

Length 105;

57

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Recombinant RaPLR1 Gln1Ser amino acid sequence.
                              AAY28870 standard; protein; 104 AA.
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                        Newton DL;
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104 AA;
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                            Rana pipiens.
                                                                                                                                                                                                                                                                                           26-MAR-1999;
                                                                                                                                                                                                                                                                                                               27-MAR-1998;
                                                                                                                                                                                                                                                   WO9950398-A2
                                                                        25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                        Rybak SM,
                                                   AAY28870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAY28871
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           RESULT 9
                      AAY2887
                                          g
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                                                             ı;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                2 NWATFQOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                            57
(Rana catesbeiana) lectin used to describe the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NWAIFQOKHIINI-PIICNTIMDNNIYIVGGQCKRVNIFIISSATIVKAICIGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                         STTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                          STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.0%; Score 282.5; DB 2;
50.0%; Pred. No. 2.3e-24;
ive 15; Mismatches 31;
                                         DB 2;
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0
                                      Score 586.5; DB 2,
Pred. No. 3.8e-59;
0; Mismatches 0;
                                                                                                                                                                                                                                                            Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                               Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                               AAW06544 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 28; 45pp; English.
                                        97.6%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                96WO-US008304.
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                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 50.0°
Matches 55; Conservative
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043063/04.
                                  Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 104 AA;
                    Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                        WO9639428-A1.
                                                                                                                                                                                                                                                                                                    Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                        22-AUG-1997
                                                                                                                                                                                                                                                                                                                                           12-DEC~1996.
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                                                                                                                                                                                                                   AAW06544;
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                                                                                                                                                                                     AAW06544
                                                                                                                                                                           RESULT
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Recombinant Rana pipiens ribonuclease; RaPLR1 Gln1Ser; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog; sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SDWLTFOKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.7%; Score 280.5; DB 2;
49.5%; Pred. No. 3.8e-24;
cive 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 34; Page 60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0079751P.
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0 61

Gaps

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0; Indels

98.3%; Score 591; DB 2; 98.2%; Pred. No. 1.2e-59; ive 2; Mismatches 0

al Similarity 98.2 107; Conservative

Query Match Best Local S

Best Loca Matches

g ਨੇ

Length 111;

3 NWATFOOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 62

TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRCP

2 NWATFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS

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Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancex; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonuclease (RacORI) protein with Met at position 1 attached to a (His) 6 tag, Met23leu and Met58Leu. Carboxy terminal end of recombinant RacORI has a covalently bound ligand binding moiety, which can be a Li2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                  TIREQLNICIRISITERPCEYSSRIEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a recombinant Rana catesbeiana oocyte
                                                                                                                                                                                                                                                                                          Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
                                                                                    62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Met not found in wild type RaCORI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                    AAY28876 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 66; 71pp; English.
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                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 23
                                                                                                                                                                                                                                                                                                                                                                                                                               catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                               Rana cates
Synthetic.
                                N
                                                                  62
                                                                                                                                                                                                                        AAY28876;
                                                                                                                                                  RESULT 6
                                                                                                                                                                      AAY28876
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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a caperific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells cytotoxic agent. The products can be used for traating cumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1. Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria cytomegalovirus) and cells infected with parasites (such as the malaria corraceptives. Finally they can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in contraceptives. Finally unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                                                                                                                                                                                                                heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; mmune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antly fused pancreatic RNase-targeting proteins useful for tumors, infections, immune or autoimmune disorders and as a
                                                                                                                                                                                                          Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Youle RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                         AAY33321 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 19; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-00510696.
91US-00779195.
93US-00014082.
                                                                                                                                                                   Frog lectin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00891848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00125462
                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-560488/47.
                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana.
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                                                                                     AAY33321;
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RESULT 7
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Sequence 111 AA;

diseases

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Gaps

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Indels

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62 19

110

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ribonuclease (RaCORI) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RaCORI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is clavated by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RacCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                              3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                    2 NWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                                                                                                   63 TTRFQLNTCTRTSITFRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.3%; Score 591; DB 2; Length 110; 98.2%; Pred. No. 1.1e-59; ive 2; Mismatches 0; Indels
                                                                                                                                 TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Wild type Met replaced with Leu"
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Mismatches
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                                                                                                                                                                                                                                                                                         AAY28874 standard; protein; 110
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  109; Conservative
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N-PSDB; AAZ08132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana.
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                                                                                                                                                                                                                                                                                                                                    AAY28874;
  Matches
                                                                                                                                                                                                                                                                    AAY28874
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                                                                                                                   61
                                                                                                                                                     NWAIFQQKHIINIPIICNIMDNNIYIVGGQCKRVNIFIISSATTVKAICTGVINMNVLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant Met(-1) Rana catesbelana oocyte ribonuclease; RaCOR1; CD22; covalently bound; LL2 antibody; ligand binding molety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
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                                                                                                              NWATEQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                     Gaps
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                                                                                                                                                                                                        TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                 62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is a recombinant Rana catesbeiana oocyte
                       Length 110;
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                                                                     Indels
                                                                         .;
0
                                              2.4e-60;
                         Score 597; DB 2;
Pred. No. 2.4e-60
             99.3%; Scc. 100.0%; Pred. No. 2... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                AAY28873 standard; protein; 111 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Met(-1) RaCOR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNase; autoimmune disease
                                                                       109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catesbeiana
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07-OCT-1999

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Synthetic

Rana

Rybak SM,

25-JAN-2000

AAY28873;

AAY28873 RESULT

62

Query Match Best Local

Matches

ð g ð d 0

Gaps

0

Conservative

Best Local Similarity

Query Match

Matches 107;

99.3%; Score 597; DB 2; Length 111; 100.0%; Pred. No. 2.4e-60;

Query Match Best Local Similarity

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Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a recombinant Rana catesbeiana ribonuclease (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end car recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-
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                                                                                                                                                                                                                                               SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMVVL 60
               terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
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                                                                                                                                                                                    Gaps
      an N-
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                                                                                                                                                                                                                                                                                                     STTRFQLNTCTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 110
Recombinant ribonucleases can be expressed in bacteria without
                                                                                                                                                     Length 110;
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                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                 Score 601; DB 2;
Pred. No. 8.2e-61;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                  AAY28878 standard; protein; 111
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                                                                                                                                                 100.0%;
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                                                                                   autoimmune diseases
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                                                                                                                                              Query Match
Best Local Similarity
Matches 110; Conserv
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                                                                                                                  Sequence 110 AA;
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                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                          2 SNWATFQQXHIINTPIICNTIMDNNIYIVGGQCKRVNFFIISSATTVKAICTGVINMNVL 61
terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana oocyte ribonuclease; RaCORI; covalently bound; CD22; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
                                                                                                                                                                                                               1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGCKRVNTFIISSATTVKAICTGVINMNVL
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
                                                                                                                                                                                                                                                                                           61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                   · (
                                                                                                                                                                                                                                                                                                                STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                 Length 111;
                                                                                                                                                                                   Indels
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                                                                                                                                             100.0%; Score 601; DB 2; 100.0%; Pred. No. 8.3e-61;
                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAY28872 standard; protein; 110
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N-PSDB; AAZ08130.
                                                                       autoimmune diseases
                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana catesbeiana
                                                                                                         Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000
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Sequence 110 AA;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model protein search, using OM protein

Run on:

May 11, 2004, 14:23:43; Search time 50.2715 Seconds (without alignments) 618.248 Million cell updates/sec

US-09-961-400-24 601 Title:

1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Perfect score: Sequence:

Scoring table:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp1980s:*geneseqp1990s:* geneseqp2001s:* geneseqp2000s:* geneseqp2002s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aay28877 Recombina				₩.	Aay28876 Recombina		-	Aay28870 Recombina			Rec				Aaw35135 R. pipien			Aaw35132 R. pipien				_	Aaw00736 Protein d	Aaw14065 Onconase
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SUMMARIES		ΩI	AAY28877	AAY28878	AAY28872	AAY28873	AAY28874	AAY28876	AAY33321	AAW06544	AAY28870	AAY28871	AAY28865	AAY28867	AAW35118	AAY28879	AAW35134	AAW35135	AAW35133	AAW35129	AAW35132	AAY28866	AAY28869	AAR12344	AAR47303	AAW00736	AAW14065
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	٠	Length	110	111	110	111	110	111	111	104	104	105	104	105	112	127	251	254	355	355	366	104	105	104	104	104	104
	* Ouery	_	100.0	100.0	99.3	99.3	98.3	98.3	97.6	47.0	46.7	46.7	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	45.5	45.5	45.3	45.3	45.3	
		Score	601	109	597	597	591	591	586.5	282.5	280.5	280.5	276.5	276.5	276.5	276.5	276.5	276.5	276.5	276.5	276.5	273.5	273.5	272.5	272.5	272.5	272.5
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AAW06543	AAW30301	AAW88233	AAY33322	AAB31666	ABG32650	AAW35123	AAY39400	AAW35122	AAW35117	AAW35125	AAW35130	AAW35126	AAW35116	AAW30302	AAB31667	ABG31617	AAW35115	AAW35127	AAW35131
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45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.2	44.8	44.5	44.5	44.5	44.5	44.5
272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	271.5	269.5	267.5	267.5	267.5	267.5	267.5
26	27	800	600	0.6	31	35	33	3.4		36	37.	ď	36.	40	4	4	4	4 4	45

## ALIGNMENTS

Recombinant Rana catesbelana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; autoimmune disease. Recombinant RaCOR1 Gln1Ser amino acid sequence. AAY28877 standard; protein; 110 AA (first entry) 25-JAN-2000 AAY28877; RESULT 1 AAY28877 

Rana catesbeiana. Synthetic.

/note= "Wild type Gln replaced with Ser" Location/Qualifiers Key Misc-difference

WO9950398-A2

07-0CT-1999

99WO-US006641. 26-MAR-1999; 98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM, WPI; 1999-610847/52.

N-PSDB; AAZ08134.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 67; 71pp; English.

The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with GlniSer. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a Liz antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

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R. Beintena J.J.;

R. Secretory Tibonolesse genes and pseudogenes in true ruminants.";

R. Gans 212.252-26 (1938).

C. C. -: SUBCENLINE LOCATIONS Secreted.

C. C. -: SUBCENLINE LOCATIONS Secreted.

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C. C. -: Substance attended through a collaboration between the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics Institute of Bioinformatics and the Swiss Institute of Swiss Institute of Bioinformatics Institutions as long as its content is in no way continued and swiss Institute of Swiss Institutions and Swiss Institutions and Swiss Institutions and Swiss Institutions and Swiss Institutions and Swiss Institutions Institution Bioinformatics Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institution Institut
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Search completed: May 7, 2004, 21:53:06 Job time : 5.60711 secs

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

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Strydom D.J., Bond M.D., Vallee B.L.,
"An angiogenic protein from bovine serum and milk -- purification and primary structure of angiogenin-2.";

Eur. J. Blochem. 247:535-544(1997).
-- FUNCTION: Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity. Has potent angiogenic activity. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.
-- TISSUE SPECIFICITY: Serum and milk.
-- SIMILARITY: Belongs to the pancreatic ribonuclease family.
HSSP: P10152: 1AGI.
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14522 MW, B703B9839919FD2F CRC64;
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Pfam; PF00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProD000535; RNaseA, 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                          Protein synthesis inhibitor; Glycoprotein;
Pyrrolidone carboxylic acid.
                                                                  MEDLINE=97409980; PubMed=9266695;
Strydom D.J., Bond M.D., Vallee B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.68;
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58

Gaps

Indels 13;

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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Giraffoidea,
Giraffidae, Giraffa.
                                                                                                                                                                                                                                                                                                                   MEDLINE=96139017; PubMed=8587129; Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M., Confolone E., Brintema J.J., Sasso M.P., Carsana A.; Palmieri M., "Molecular evolution of genes encoding ribonucleases in ruminant species.";
029542; 029533;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB)
                                                                                             141 AA
                                                                                           PRT;
                                                                                                                                                                                                      Giraffa camelopardalis (Giraffe).
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                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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           SEQUENCE OF 31-114 FROM N.A.
MEDLINE=93367815; PubMed=8360916;
Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
Carsana A., Palmieri M., Furia A.;
"Sequences related to the ox pancreatic ribonuclease coding region in the genomic DNA of mammalian species.";
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    J. Mol. Evol. 37:29-35 (1993).
    -!- SUBCELLULAR LOCATION: Secreted.
    -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                         P87350;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                   151 AA.
                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetar
Cervidae; Cervinae; Axis.
                                                STANDARD;
                                                                                                                                                                                                                Axis porcinus (Hog deer)
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                                              RNBR AXIPR
RESULT 15
RNBR AXIPR
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Beintema J.J.;
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                                                      5 ATFQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 58
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                                                                                                        32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK
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  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonuclease.";
1. Eur. J. Biochem. 219:641-646(1994).
2. CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
2. SUBCELIDIAR LOCATION: Secreted.
3. SUBCELIDIAR LOCATION: Secreted.
4. SIMILARITY: Belongs to the pancreatic ribonuclease family.
3. PIR: 54111.
34111.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana.
NCBI TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid. MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao W., Beintema J.J., Hofsteenge J.; "The amino acid sequence of ignana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 119;
  43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
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6072FB5B7B15BD5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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18;
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     37; Conservative
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RESULT 12

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 NITCKNGQPNCYQSNSTMNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 NVL------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AKERRQHMDSGSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Raibonuclease, brain (EC 31.27.-) (BRB).
Capreolus capreolus (Roe deer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocolleinae; Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                 "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 !- SIMILARITY: Belongs to the pancreatic ribonuclease family
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O-LINKED (GLCNAC. . . . ) (BY O-LINKED (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Muclease; Endonuclease; Glycoprotein. ACT_SITE 41 8Y SIMILARITY.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ANG2.
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151 AA
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PRT;
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133 0-
16971 MW;
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ProDom; PD000535; RNaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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PROSITE; PS00127; RNASE_PAN
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STANDARD;
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151 AA;
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Best Local Similarity
Matches 34; Conserv
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us-09-961-400-21.rsp

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16-0CT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
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                                                                                                                                                                Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J., "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 PQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NGQINCYQSNSTMHITDCRQIGSSKYPNCAYKASQEQKHIIVACEGNPPVPHF 120
                                                                                                                                                                                                                                                                                     3'-
U-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VLSTTRFQLNT-----CTRISITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                               Sus scrofa (Pig).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                     J. Biol. Chem. 245:654-661 (1970).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2', 3'-cyclic phosphate intermediates.

-!- SUBCELLULAR LOCATION: Secreted.
-!- TASUE SERECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; A92071; NRPG.
-- HSSP; P00656; ISRN.
                                                                                                    Jackson R.L., Hirs C.H.W.;

"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";

J. Biol. Chem. 245:637-653 (1970).
                                                                                                                                                                                                                             MEDLINE=70104198; PubMed=4904878; Phelan J.J., Hirs C.H.W.; "The primary structure of porcine pancreatic ribonuclease. 3. dissilfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 129.5; DB 1; Length 124;
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
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N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
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PRIMT; PR00074; rnaseA; 1.
PRIMTS; PR00794; RIBONUCLEASE.
ProDom; PD000515; RNaseA; 1.
SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PanCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.4%; Score 129.5; -- 30.7%; Pred. No. 4.1e-07; rive 20; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 AA
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                                                                                            MEDLINE=70104197; PubMed=5460946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13804 MW;
                                                                                                                                                                                                 FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Conservative
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DISULFIDE BONDS.
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                    RNASE1 OR RNS
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(Rel. 31, Created)
(Rel. 31, Last sequence update)

P39873; 01-FEB-1995 01-FEB-1995

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                                                                                                                                                                                                          Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S., Viola M., Palmieri M., Russo E., Furia A.; "Molecular cloning of the gene encoding the bovine brain ribonuclease and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474(1991).
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
Obji K., Irie M.;
"Primary structure of a ribonuclease from bovine brain.";
J. Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vento M.T., Furia A.; "Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.
Vento M.T., Furia A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Evol. 41:850-858 (1995).
- SUBCELLULAR LOCATION: Secreted.
- SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 129.5; DB 1; Length 167; Pred. No. 5.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PROPORT, PD000535; NARes eP.; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> S (IN REF. 2).
681CAAC3CC2FC459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. /FTId=CAR_000005.
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                                                                                                                                                                                      MEDLINE=92093604; PubMed=1754384;
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X59767; CAA42439.1; -. EMBL, S81744, AAB36138.1; -. PIR; S20066; S20066. HSSP, P00656; 2RNS. GlycosuteDB, F39873; -. InterPro; IPRO1427; RNSS-PIEM, PF00074; rnaseA; 1.
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Bos taurus (Bovine).
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167 AA;
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63 CKDVNTFIHGNKSNIKAICGANGSPYRENIR-MSKSPFQVTTCKHTGGSPRPFCQYRASA 121

88 ETNYICVKCENQYPVHF 104 :::||||||| 122 GFRHVVIACENGLPVHF 138

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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N. Krzywinski M.I., Skalka W.A.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 1162:177-186 (1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00092; RNASe_Pc; 1.
RNOSITE; PS00127; RNASE_PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93192291; PubMed-8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
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                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
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EMBL; BC055355; AAH55355.1;
PIR; A35932; A35932.
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64
137
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145 AA;
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                                                                                                                                                                                                                                                       3'-
U-P
                                                                                                                                                                                     MEDLINE=76277855; PubMed=962870;
Emmens M., Welling G.W., Beintema J.J.;
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                          Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                        Biochem. J. 157:317-323 (1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphoolisgonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .) (30%).
                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
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                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNAGE PC; 1.
PROSITE; PS00127; RNAGE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.7%; Score 131.5; DB 1
32.5%; Pred. No. 2.5e-07;
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124 AA
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PRT;
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HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14125 MW;
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                 NCBI_TaxID=9767;
                                                                                                                                                                                                                               ribonuclease.";
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3;

Gaps

7;

Indels

28;

22.6%; Score 136.5; DB 1; Length 145;

Pred. No. 8.4e-08;

40.3%;

31; Conservative

Matches

Best Local Similarity

Query Match

11; Mismatches

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-!- SIMILARITY: Belongs to the pancreatic ribonuclease family
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MOD_RES
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129; TISSUB=Liver; MEDLINE=96079109; PubMed=8530072; MEDLINE=96079109; PubMed=8530072; Brown W.E., Nobile V., Subramanian V., Shapiro R.; "The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes."; Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                  Mol. Cell. Biol. 17:1503-1512(1997).
-!- FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; FDUVOSS, RNASE PC; 1.
SMART; SM0092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
24
Protein synthesis inhibitor; POTENTIAL.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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(BY SIMILARITY).
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developmentally regulated genes when expressed in NIH 3T3
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ProDom; PD000535; RNaseA; 1.
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Pfam; PF00074; rnaseA; 1.
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145 AA;
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                       fibroblasts."
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=FVB/N, TISSUE=Liver;
MEDLINE=22388257; PubMed=124.7932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Ol-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID (BY
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9; Mismatches 27; Indels
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MEDLINE=91025023; PubMed=2222458;
MEDLINE=91025023; Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
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Pyrrolidone carboxylic acid.
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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InterPro; IPR001427; RNaseA.
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ANG3 OR ANGL.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94166079; PubMed=8120892; Mesimann S.C., Ardelt W., James M.N.G.; Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity."; J. Mol. Biol. 236:1141-1153 (1994).
                                                                    MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens
occytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                  60 VESTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                              61 ELSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
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J. Biochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2'.3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR, 2X0085, 7X0085.
HSSP; P11916, 1BC4.
InterPro, IPR001427; RNaseA.
PFERM; PF00074; rnaseA.
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Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                         Length 111;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                          61.2%; Score 370; DB 1; Lularity 64.9%; Pred. No. 4.4e-33; Conservative 10; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) P-30 protein (EC 3.1.27.-) (Onconase). Rana pipiens (Northern leopard frog).
                                                                                                                                                                                                                                                                                                                                                                  104 AA
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Proteins 14:392-400(1992).
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ses 72; Conserv
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P22069;
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Matches
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1 ODWITFOKKHITNIRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
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FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high
                                                                                          molecular weight ribosomal RNA.
-1- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, List annotation update)
Anglogenin-3 precursor (EC 3.1.27.-) (Anglogenin-related protein
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48.6%; Pred. No. 1e-22;
ive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                SMART: SW00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
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MEDLINE=97184476; PubMed=9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11845 MW;
                                                                                                                                                                                        PDB; 10NC; 31-JAN-94.
Interpro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 48.6
nes 54; Conservative
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglinates various animal cells, including normal lymphocyces, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1BC4; 28-OCT-98.
PDB; 1MO7; 21-JAN-03.
PDB; 1MO7; 21-JAN-03.
PIT terPro; 1PR001427; RNaseA.
PEAM; PF00074; MaseA; 1.
ProDom; PD000535; RNaseB.; 1.
SWART; SW00092; RNASE PC; 1.
PROSTE; PS00127; RNASE PRICKEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ONWATFQOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 133;
                                                                                                                                                                                                                                                                                                  RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14762 MW; A7D62594F7D16F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 585.5; DB 1;
Pred. No. 3.2e-56;
2; Mismatches 0;
                                                                                                                                                                                                                                                                          EMBL; AF039104; AAD10702.1; -.
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                                                            SUBUNIT: Monomer.
                                                                                                                                                                                        PIR; A27121; A27121
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133 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Last sequence update)
Last annotation update)

Created)

LECS RANJA P18839; 01-NOV-1990 01-FEB-1994 10-OCT-2003

LECS_RANJA

ID LECS_RA

AC P18839;

DT 01-NOVDT 01-FEBDT 10-OCT-

RESULT 2

16, 28, 42,

(Rel.

111 AA

PRT;

STANDARD;

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59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN
                                                                                                                                                                                                                                                                                        -i- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
-i- SUBGNIT: Monomer.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
MEDLINE=90130374; PubMed=2613682;
Nitte R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Nokazaki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                  Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.;
Takayanagi Y., Titani K.;
"Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                 Rana japonica (Japanese reddish frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 451; DB 1; Length 11
Pred. No. 8.1e-42;
8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000555; RNaseA; 1.
SMART; SM00092; RNASE PACEATIC; 1.
PROSITE; PS00127; RNASE PANCEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12326 MW; FDEBDDF3834ED679 CRC64;
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01-FRB-1994 (Rel. 28, Last sequence update)
16-FRB-2003 (Rel. 41, Last annotation update)
Ribonuclease, liver (EC 3.1.27.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Sialic acid-binding lectin (EC 3.1.27.-).
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                                                                                                                                                                 MEDLINE=91035319; PubMed=2229005;
                                                                                                                       SEQUENCE, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                       eggs.";
J. Biochem. 108:139-143(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JX0120; JX0120.
HSSP; P11916; 1BC4.
InterPro; IPR001427; RNaseA.
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77.5%;
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MOD RES 1
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                                                                                 NCBI_TaxID=8402;
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104
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Best Local
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2,

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2004, 21:30:40; Search time 5.60711 Seconds (without alignments) 1030.796 Million cell updates/sec Run on:

US-09-961-400-21 605 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ָרָ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִרְ בְּיִבְּיִים בְּיִבְּיִבְּיִים בְּיִבְּיִבְּיִבְּיִם בְּיִבְּיִבְּיִבְּיִבְּיִבְּיִבְּיִבְּיִ	Mesci in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the c	rana	rana	6 rana	P22069 rana pipien	mus m	Q64438 mus musculu	mus	P00673 balaenopter	P00671 sus scrofa		37	_				Q8wn65 miopithecus		Q8wn66 cercopithec				P31346 sus scrofa			Q8wn62 saguinus oe		P00683 mus musculu	'n	P00679 cavia porce	N	0	00674	P03950 homo sapien
SUMMARIES	£			LECS_RANJA		RN30 RANPI	ANG3 MOUSE	ANGR_MOUSE	ANGI MOUSE	RNP BALAC	RNP_PIG	RNBR BOVIN	RNP_IGUIG	RNBR_CAPCA	ANG2_BOVIN	RNBR_GIRCA	RNBR_AXIPR	ANGI_MIOTA	ANGI_SAISC	ANGI_CERAE	ANGI_PONPY	RNBR_SHEEP	RNP_MACRU	ANGI_PIG	RNP_ANTAM	ANGI_AOTTR	ANGI SAGOE	RNP_MYOCO	RNP MOUSE	ANGI_MACMU		ANGI_BOVIN	RNP_CAMDR		ANGI_HUMAN
	T.ength	- 1	133 1									167 1					151 1						122 1									œ	4	128 1	147 1
d	Query Match		8.96	74.5	61.2	45.2	25.5	24.7	22.6			21.4	21.1	20.6		20.4	20.4	20.3	20.3	19.8	19.8	19.8	19.7	on	19.6	O1	19.3	19.3	19.3	19.0	18.9	œ,	18.8	œ,	18.7
	0 1	•	585.5	451	370	273.5	154.5	149.5	136.5	131.5	129.5	129.5	127.5	124.5	123.5	123.5	123.5	123	123	120	120	119.5	119	118.5	118.5	118	117	116.5	116.5	115	114.5	114	ω.	113.5	113
	Result		ı	7	e	4	S	9	7	හ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q8wme8 pan troglod	P04059 proechimys P00666 rangifer ta	Q8wn64 papio hamad Q9jjh1 mus musculu	P31347 oryctolagus P00664 capreolus c	P00662 giraffa cam P24717 cricetulus	P00657 bubalus bub Q9wuv5 peromyscus
ANGI_PANTR RNS4_ROVIN	RNP FROGU	ANGI PAPHA RNS4 MOUSE	ANGI_RABIT RNP_CAPCA	RNP_GIRCA RNP_CRILO	RNP_BUBBU RNP_PERLE
П.		н н	п п		пп
147	128	146 148	125	124 130	124 148
18.7	18.6 18.1	18.1	18.0	17.9	17.8
113	112.5	109.5	109	108.5	107.5
3.4 7.4	3.6	3.8	40	4 24 3	44 45

# ALIGNMENTS

RESULT 1  RNPO RANCA  TD RNPO RANCA STANDARD; PRT; 133 AA.  AC P11916; Q9PWR7;  DT 01-OCT-1989 (Rel. 12, Created)  DT 10-OCT-2003 (Rel. 42, Last sequence update)  DT 10-OCT-2003 (Rel. 12, Last sequence)	Ribonuclease, oocytes precubinding lectin) (SBL-C). RCR. RCR. RCRana catesbeiana (Bull frog Rana catesbeiana (Bull frog Ruphibia; Batrachia; Anura, NCBI_TaxID=8400;	RN [1] RP SEQUENCE FROM N.A.  RC TISSUE-Liver;  RX MEDLINE-98165825; PubMed-9497370;  RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;  RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.  RT Tissue distribution, cloning, purification, cytotoxicity, and active  RT residues for RNase activity.";  RT J. Biol. Chem. 273:6395-6401 (1998).	RD SEQUENCE OF 23-133.  RC TISSUE=E9G;  RX MEDIANE=87299649; Pubmed=3304421;  RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,  RA Takayanagi G., Hakomori S.;  RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) e9gs.";  RB Biochemistry 26:2189-2194(1987).  RN GARACTERIZATION, AND SEQUENCE OF 81-101.  RX MEDIANE=22226613; Pubmed=137327;		RL Glycobiology 3:37-45(1993).  RN [5]  RN STRUCTURE BY NMR OF 23-133.  RX MEDLINE=98437383; PubMed=9761686;  RA Chang CF., Chen C., Chen YC., Hom K., Huang RF., Huang T.H.;  RT The solution structure of a cytotoxic ribonuclease from the occytes  RT TR catesbeiana (bullfrog).";  Of Rana catesbeiana (bullfrog).";  LJ Mol. Biol. 283:231-244(1999).  CC -:- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
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pancreatic ribonuclease (BC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Accession: A00826
C;Accession: A00826
R;van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases: Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 FOOKHI-----INTPLICNTILDNNIYIVGGOCKRVNIFILSSATIVKALCTGVINLNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --INTPLICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STIRFOLNICIRISITPRP-CPYSSRIEINYICVKCENQ--YPVHF 104
                                                                                                                    --STIRFQLNICIRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A00826
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: notein
A; Note: 64-Pro was also found
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 21, 44/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.8%; Pred. No. 0.00024;
Matches 36; Conservative 15; Mismatches 43; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 7, 2004, 21:54:56 Job time: 10.072 secs
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pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
C;Accession: A34090; S22598; A00830
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
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K;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A;Reference number: S22598; MUID:92107684; PMID:1840677
                                                                                                                                                                                                                 of coypu and chinchilla pancreatic
                            C;Species: Myocastor coypus (nutria, coypu)
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
B;Van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pan A;Reference number: A90612; MUID:77065676; PMID:999896
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Reference number: A90612; MUID:77065676; PMID:999896
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A; Residues: 1-149 < SAM>
A; Residues: 1-149 < SAM>
A; Residues: 1-149 < SAM>
A; Residues: 1-149 < SAM>
A; Cross-references: EMBL:X60103; NID:953981; PIDN:CAA42697.1; PID:953982
B; Lengtra, J.A.; Beintema, J.J.
Bur. J. Biochem. 98, 399-408, 1979
A; Title: The amino acid sequence of mouse pancreatic ribonuclease.
A; Reference number: A00830; MUID:80024269; PMID:556267
A; Accession: A00830
A; Molecule type: protein
A; Residues: 26-149 < LEN>
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancrease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancrease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; Pancreatic ribonuclease #status experimental < R37, 66, 1447 Active site: His, Lye, His #status predicted
F;51-109, 66-120, 83-135, 90-97/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 FQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 116.5; DB 1
30.8%; Pred. No. 0.00015;
ive 16; Mismatches 42
          N; Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.3
Best Local Similarity 30.8
Matches 36; Conservative
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Matches 35; Conserv
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A; Residues: 1-149 <SCH>
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A; Status: preliminary
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Cispecies: Antilocapra americana (pronghorn)
Cispecies: As Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
Ciscossion: A00813
Ribeintema, J.J.; Gaastra, W.; Munniksma, J.
Ribeintema, J.J.; 305-316, 1979
A.Title: Brod. 13, 305-316, 1979
A.Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse angiogenins: discernme
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                                                                                                                                                                                                                                                                                                        angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S29834; A43825
R;Bord, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 116,2, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenin
A;Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKNGQINC-YQSYSIMSIIDCREIGSSKYPNCAYKTIQAKKHIIVACEGNPYVPVHY 120
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                                                                                                                53 TGVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 104
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N;Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the Protein Sequence Database, ribonuclease
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A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 123;
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Pred. No. 9.2e-05;
6; Mismatches 35
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A; Residues: 1-123 <BON>
A; Note: this sequence was
C; Superfamily: pancreatic
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Best Local Similarity
Matches 35; Conserv
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A; Status: preliminary
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paraceatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Species: Iguana iguana (common iguana)
C;Species: Iguana iguana (common iguana)
C;Species: Iguana-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111
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NiAlternate names: RNase 1; RNase A
CiSpecies: Macropus rufus, Megaleia rufa (red kangaroo)
CiStes: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accesion: A00833
R;Gastra, W.; Welling, G.W.; Beintema, J.J.
Bichem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accesion: A00833
A;Molecule type: protein
A;Residues: 1-12. ccAAA.
C;Superfamily: pancreatic ribonuclease
C;Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His. Lyg, His #status predicted
F;55-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
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                                                                                                                                                                                                                                                                                                                            59 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
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                                                                                                                                                                5 ATFQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL
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                                                                                    Gaps
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    Query Match 21.4%; Score 129.5; DB 2; Best Local Similarity 30.6%; Pred. No. 1e-05; Matches 37; Conservative 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.7%; Score 119; DB 1;
29.8%; Pred. No. 8.2e-05;
iive 17; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.1%; Score 127.5; DB 2 29.6%; Pred. No. 1.1e-05; ive 17; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::
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R;Watanabe, H.; Katch, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Irri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
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A;Molecule type: protein
A;Residues: 1, 0, 3-124 cJAC>
R;Wierenga, K.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
                                                                                                                                                                                                                                                                                      amino acid
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A; Residues: 1-124 <WIE>
B; Phelan, J. J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A; Title: The primary structure of porcine pancreatic ribonuclease. III. The A; Reference number: A92072; MUID:70104198; PMID:4904878
A; Contents: annotation; disulfide bonds
G; Superfamily: pancreatic ribonuclease
G; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 12, 34, 76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status experimental
                             NyAlternate names: RNase 17, Names 17, Names 18, State names: RNase 17, RNase A C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: A-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C; Accession: A92071, A91391; A00816
R; Jackson, R.L.; Hirs, C.H.W.
J; Biol. Cham. 245, 637-653, 1970
J; Biol. Cham. 245, 637-653, 1970
A; Fitle: The primary structure of porcine pancreatic ribonuclease. II. The A; Reference number: A92071; MUID: 70104197; PMID: 5460946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 NGQINCYQSNSTMHIIDCRQIGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
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C, Keywords: glycoprotein, hydrolase
F;38 67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Bhinding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4%; Score 129.5; DB 1 30.7%; Pred. No. 7.6e-06; iive 20; Mismatches 42
pancreatic ribonuclease (EC 3.1.27.5)
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A;Residues: 27-154,'8',156-166 <WAT>
A;Experimental source: brain
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Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-167 <SAS>
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N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mis musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Andleoule type: DNA
A;Residues: 1-145 <BON>
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Genetics:
A;Introns: angiogenesis: hydrolase; nucleic acid degradation; pyroglutamic acid
C;Reywords: angiogenesis: hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64;137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted
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Cispecies: Balaenoptera acutorostrata (minke whale, lesser rorqual)
Cispecies: Balaenoptera acutorostrata (minke whale, lesser rorqual)
Cispecies: Balaenoptera acutorostrata (minke whale, lesser rorqual)
Cispecies: Balaenoptera acutorostrata (minke whale, lesser rorqual)
Biochem. J. 157, 317-323, 1976
Airtle: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
Airtle: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
Aireference number: A00818; MUID:76277855; PMID:962870
Airesidues: 1-124 < FEMA.
Cisuperfamily: pancreatic ribonuclease
Circywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
Circywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
Fill, A1,119/Active site: His, Lys, His #status predicted
Fill, A1,109/Active site: His, Lys, His #status predicted
Fill, B1,100,65-72/Disulfide bonds: #status predicted
Fill, B1,100,65-72/Disulfide covalent) (partial) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 22.6%; Score 136.5; DB 1; Length 1 Similarity 40.3%; Pred. No. 1.8e-06; 31; Conservative 11; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic ribonuclease (EC 3.1.27.5) - minke whale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 ETNYICVKCENQYPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: : ||| ||||
122 GFRHVVIACENGLPVHF 138
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Best Local Similarity
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C;Species: Rana pipiens (northern leopard frog)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mixulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Accession: A39035
A;Bettern proliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.; Abe, Y.; Okazaki, T.; Ohg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rana catesbeiana) liver.
                                                                                                                                                                                                                                                                                                                                                                               Dancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: UX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) 1i
A;Reference number: UX0085; MUID:90130374; PMID:2613682
A;Accession: UX0085
A;Molecule type: protein
A;Residues: 1-111 < NUTP
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyrolidane carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: pyrrolidane carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
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O
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                                               OWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN
              QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ONWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ONWATFQOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENOAPVHFVGVGSC
                                                                                                                                                     VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC
                                                                                                                                                                                             27; Indels
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Pred. No. 1e-29;
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64.98;
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Matches 53; Conserv
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RESULT 5

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OM protein - protein search, using sw model

Run on:

May 7, 2004, 21:38:36; Search time 10.072 Seconds (without alignments) 1060.090 Million cell updates/sec

US-09-961-400-21 605 1 MQNWATFQQKHIINTPIIGN.....ICVKCENQYFVHFAGIGRCP 111 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	ribonuclease-relat	ribonuclease-relat	pancreatic ribonuc	ribonuclease-relat	angiogenin precurs		pancreatic ribonuc	pancreatic-type ri	pancreatic ribonuc	pancreatic ribonuc	anglogenin - pig		pancreatic ribonuc	pancreatic ribonuc	_	angiogenin [valida		pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	angiogenin precurs	pancreatic ribonuc	ribonuclease - dom	pancreatic ribonuc	angiogenin - rabbi	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc
CHANGE	ID	A27121	JX0120	JX0085	A39035	A35932	NRWHK	NRPG	S20066	S41111	NRKGR	A43825	NRPRH	NRCU	NRMS	NRGPB	A32474	NRCM	NRCMM	NRCMB	NRHO	NRHUAG	NRKS	S08549	NRDEN	B43825	NRGF	NRDEO	S22808	NRWB
	ength DB	111	111 1			145 1	4	124 1						128 1	149 1	128 1	•	124 1									_		130 2	124 1
%∙	Query Match Length	9	74.5	61.2	4.	22.6	21.7	21.4	21.4	21.1	19.7	19.6	19.6	19.3	19.3	18.9	18.8	18.8	18.8	18.8	18.8	18.7	18.6	18.3	18.1	18.0		17.9	17.9	17.8
	Score	582.5	451	370	270.5	136.5	131.5	129.5	129.5	127.5	119	118.5	118.5	116.5	116.5	114.5	114	113.5	113.5	113.5	113.5	113	112.5	110.5	109.5	109	108.5	108.5	108.5	107.5
	Result No.	 	7	m	4	5	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

eosinophil-derived pancreatic ribonuc	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc	seminal ribonuclea	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc
I61900 NRBOB	NREKN S07141 NREC	JX0115 NRSH	NRRT	A47498 NPBOS	NRHP S04503	NRGN	S08546
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158	124	119	152	125	124	124	124
17.8	17.6	17.4	17,4	17.1	16.9	16.6	16.6
107.5	106.5	105.5	105.5	103.5	102.5	100.5	100.5
30	8 8 8 2 8 8	3 3 3	37	9 6 4	444	4 4 4	45

# ALIGNMENTS

RESULT 1 A27121 ribonuclease-related sialic acid-binding lectin - bullfrog C;5cocies: Rana catesbelana (bullfrog) C;5accies: Rana catesbelana (bullfrog) C;5accies: Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993 C;5accion: A27121 R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag R;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbelana) A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbelana) A;Reference number: A27121 A;Molecule type: protein A;Mesidues: 1-11 < TIT> C;Superfamily: panoreatic ribonuclease C;Keywords: lectin
 Query Match         96.3%;         Score 582.5;         DB 2;         Length 111;           Best Local Similarity 96.4%;         Pred. No. 9.5e-51;         Indels 1;         Gaps 1;           Matches 107;         Conservative 3;         Mismatches 0;         Indels 1;         Gaps 1;           QY         2 QNWATFQQKHINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINLANV 60         LinmalFQQKHINTPIINTPIINTVINTYINGQCKRVNTFIISSATTVKALCTGVINMANV 60           QY         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPWHFAGIGRCP 111           Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPWHFAGIGRCP 111
RESULT 2 JX0120 ribonuclease-related sialic acid-binding lectin - Japanese frog C;Becies: Rana japonica (Japanese frog) C;Becies: Rana japonica (Japanese frog) C;Accession: JX0120 R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi J; Biochem. 108, 139-143, 1990 A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs. A;Accession: JX0120 A;Accession: JX0120 A;Molecule type: protein A;Residues: 1-11, cKAM. A;Besidues: 1-11, cKAM. A;Experimental source: egg C;Superfamily: pancreatic ribonuclease C;Keywords: lectin; pyrcollutanic acid E;1,Mobified site: pyrrolidone carboxylic acid (Gln) #status experimental F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental
 Query Match  Best Local Similarity 77.5%; Pred. No. 1e-37;  Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

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Query Match 47.0%; Score 284.5; DB 10; Length 111;
Best Local Similarity 50.0%; Pred. No. 1.9e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps
; ORGANISM: Rana pipiens
US-09-961-400-9
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Search completed: May 7, 2004, 21:51:59 Job time : 36.6155 secs

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GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
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APPLICAMY: COLDENBERG, DAVID M.
APPLICAMY: COLDENBERG, DAVID M.
APPLICAMY: NEWTON, DIANNE L.
FITTED OF INVENTION: IMMUNCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1059
CURRENT APPLICATION NUMBER: 08/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
                                               2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
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                                                                                                                                             63 TIRFOLNICIRISITPRPCPYSSRIEINYICVKCENOYPVHFAGIGRCP 111
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Pred. No. 2.9e-59;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09961400 Publication No. US20030124131A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.2%;
Matches 107; Conservative 2
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ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                       US-09-961-400-24
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LENGTH: 111
TYPE: PRT
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OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
OTHER INFORMATION: (recombinant RaCORI Q1S)
US-09-948-3918-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RacORI OTHER INFORMATION: Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110;
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; Sequence 24, Application US/09948391A
; GRUERAL INFORMATION:
   APPLICANT: Nybak, Susanna M.
   APPLICANT: Newton, Dianne L.
   APPLICANT: The United States of America
   APPLICANT: The United States of America
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   APPLICANT: Department of Health and Human Services
   FILE REFERENCE: 015280-343110US
   CURRENT APPLICATION NUMBER: US 60/079,751
   PRIOR APPLICATION NUMBER: WO PCT/US99/06641
   PRIOR APPLICATION NUMBER: WO PCT/US99/06641
   PRIOR APPLICATION NUMBER: US 09/622,613
   PRIOR APPLICATION NUMBER: US 09/622,613
   PRIOR APPLICATION NUMBER: 200-08-17
   NUMBER OF SEQ ID NOS: 43
   NUMBER PETRING DATE: 200-08-17
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor Rnase
FILE REFERENCE: 015280-3431100/S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
FRIOR PAPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 2000-08-17
PRIOR PELICATION NUMBER: US 09/622,613
PRIOR PELICATION NUMBER: US 09/622,613
PRIOR PELICATION NUMBER: US 09/622,613
PRIOR PELICATION NUMBER: US 09/622,613
PRIOR PELICATION NUMBER: US 09/622,613
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PRIOR PELICATION NUMBER: US 09/622,613
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PRIOR PELICATION NUMBER: US 09/622,613
PRIOR PELICATION NUMBER: US 09/622,613
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Pred. No. 1.3e-59;
0; Mismatches 1;
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.1%;
Matches 109; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.2
Matches 107; Conservative
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Best Local Similarity
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LENGTH: 110
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ORGANISM: Artificial Sequence
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Best Local Similarity 97.3%;
Matches 108; Conservative
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Matches 108; Conservative
                                                TYPE: PRT
ORGANISM: Rana catesbeiana
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                                                                                                       US-09-961-400-26
SEQ ID NO 26
LENGTH: 111
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Sequence 26, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: WEARK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALICHANT:
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFRENCE: 018033/1059
CURRENT APPLICATION NUMBER: 09/62,613
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
  QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
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Pred. No. 7.9e-60;
2; Mismatches 1; Indels
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CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W5 60/079,751
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: PALENTIN Ver. 2.00
SEQ ID NO 26
                                                                                                                                                                                                                                         Sequence 26, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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Best Local Similarity 97.3%;
Matches 108; Conservative
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US-09-961-400-26
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                                                                                                                                                                                                                                                     61 LSTTREQLNTCTRTSITPRECPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
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Length 111;
                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Newton, Dianne M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO 90/622,613
PRIOR APPLICATION NUMBER: WO 99/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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The United States of America
as represented by The Secretary of the
Score 596; DB 10;
Pred. No. 7.9e-60;
2; Mismatches 1;
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2 ONWAIFQOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
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Publication No. US20030124131A1
EBBEAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GGLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbeiana occyte ribonuclease (RaCORI) synthetic
OTHER INFORMATION: gene modified to use E. coli preferred codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 STIRFQLNICTRISITPRECPYSSRIEINYICVKCENQYPVHFAGIGRCP 111
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                                             APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1099-03-26
PRIOR FILING DATE: 1090-03-16
STROK FILING DATE: 1090-03-17
STROK FILING DATE: 1090-03-16
STROK FILING DATE: 1090-03-16
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STROK FILING DATE: 1090-03-17
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FILE REPREBACE: 01273/LOS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRICR APPLICATION NUMBER: 09/622,613
PRICR APPLICATION NUMBER: PT/US99/06641
PRICR APPLICATION NUMBER: PCT/US99/06641
PRICR APPLICATION NUMBER: PCT/US99/06641
PRICR APPLICATION NUMBER: 60/079,751
PRICR PILING DATE: 1998-03-26
PRICR PILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                Rybak, Susanna M.
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Best Local Similarity
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US-09-961-400-15
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Best Local S:
Matches 108
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Sequence 19, Application US/09961400
| Publication No. US20030124131A1
| GENERAL INFORMATION: US20030124131A1
| APPLICANT: RYBAK, SUSANNA M.
| APPLICANT: RYBAK, SUSANNA M.
| APPLICANT: RYBAK, DAVID M.
| APPLICANT: NEWTON: INMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT ITILE OF INVENTION: CELLS
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION: UMBER: US/09/961,400
| CURRENT FILING DATE: 2001-09-25
| WRICK APPLICATION NUMBER: 09/622,613
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| NUMBER OF SEQ ID NOS: 43
| SECTUMARE PREDETION VOICE: 1099-03-26
| NUMBER OF SEQ ID NOS: 43
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Pred. No. 2.1e-60;
2; Mismatches 0, Indels
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99.2%; Score 600; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.7e-60;
Matches 110; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1909-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
SOFTWARE: PALENTIN NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
SOFTWARE: PALENTIN Ver. 2.1
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98.2%;
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US-09-961-400-19
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US-09-948-391A-15
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LENGTH: 110
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ORGANISM: Artificial Sequence
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US-09-961-400-22
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US-09-961-400-17
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: LOSIS 33/1059
TURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/52,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PAPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATCHIL VOF: 2.1
SEG ID NOS: 43
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1 MONWATFOOKHIINTPIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINLNV
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| Sequence 22, Application US/09948391A
| Publication No. US20030027311A1
| GENERAL INFORMATION:
| APPLICANT: Rybak, Susanna M.
| APPLICANT: The United States of America
| APPLICANT: The United States of America
| APPLICANT: The United States of America
| APPLICANT: Department of Health and Human Services
| TITES OF INVENTION: Recombinant Anti-Tumor Rhase
| TITES OF INVENTION: Recombinant Anti-Tumor Rhase
| FILE REFERENCE: 015280-343110US
| CURRENT APPLICATION NUMBER: US 60/079,751
| PRIOR FILING DATE: 1999-03-27
| PRIOR FILING DATE: 1999-03-27
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 2000-08-17
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATENTION VERSE: US 09/622,613
| FROM FILING DATE: 2000-08-17
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATENTION VERSE: US 09/622,613
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Pred. No. 7.5e-61;
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; ORGANISM: Rana catesbeiana
US-09-961-400-21
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Matches 111; Conservative
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US-09-948-391A-22
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Best Local 8
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APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: MEMPON, DIAANB L.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS.

FILE REFERENCE: 018733/1059;
CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR PILING DATE: 2000-08-17

PRIOR PILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 2: 2

LENGTH: 117
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Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:Rana
CTHER INFORMATION: catesbelana ribonuclease with (His)6 tag, Met at
CHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
CTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
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ilarity 100.0%; Pred. No. 8e-61;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09961400 Publication No. US030124131A1 GENERAL INFORMATION: APPLICANT: RYBAK, SUSANNA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rana catesbeiana
US-09-961-400-22
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nes 111; Conserv
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GenCore version 5,1.6 (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:29:40 ; Search time 35.6155 Seconds (without alignments) 865.070 Million cell updates/sec May Run on:

605 1 MONWAIFQQKHIINTPIICN.....ICVKCENQYEVHFAGIGRCP 111 US-09-961-400-21 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1140673 seqs, 277566755 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

| Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/DS07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.ppp:*
Published Applications AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Seguence 21. Appl	21,		22	17.	19,	15,	15,	26,	26.	17,	19	24	24	9, 'A
		Dei				•,	~,		••	02	0,	0,	0,	0,	0,1	0,	. 02
SUMMARIES		ID	US-09-948-391A-21	US-09-961-400-21	US-09-948-391A-22	US-09-961-400-22	US-09-961-400-17	US-09-961-400-19	US-09-948-391A-15	US-09-961-400-15	US-09-948-391A-26	US-09-961-400-26	US-09-948-391A-17	US-09-948-391A-19	US-09-948-391A-24	US-09-961-400-24	US-09-961-400-9
		DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
		Query Match Length DB	111	111	117	117	111	110	110	110	111	111	111	110	110	110	111
	٥ķ٥	Query Match	100.0	100.0	100.0	100.0	99.3	99.5	98.5	98.5	98.5	98.5	98.3	98.5	7.76	97.7	47.0
		Score	605	605	605	605	109	009	596	296	296	296	595	594	591	591	284.5
		Result No.	н	7	m	4	S	9	7	8	σ	10	11	12	13	14	15

Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 2, Appli	23,13	Sequence 28, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 11, Appli	1, 9, 1, 1	3, Ap. 3, Ap. 3, Ap. 2, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 103, Ap. 10	139, 141, 254, 254, 58,
10 US 10 US 10 US 14 US	10 US 10 US 10 US 10 US	10 US-09-961-400-28 10 US-09-948-391A-2 10 US-09-948-391A-4 10 US-09-961-400-4 10 US-09-961-400-4		12 9 10 10 12 12 12	15 US-10-074-978A-139 15 US-10-074-978A-141 9 US-09-731-872-254 10 US-09-876-997-254 12 US-10-461-713-58 13 US-10-016-447-5
46.7 105 46.7 105 46.5 105 46.0 105	5.9 105 5.9 105 5.9 105 5.9 127	5.7 104 5.7 104 5.7 104 5.0 104	45.0 105 45.0 105 45.0 111 44.4 104 44.4 104	<b></b>	21.1 119 19.5 99 19.3 147 19.3 147 18.8 123 18.8 124
	277.5 277.5 4 277.5 4 277.5		272.5 272.5 272.5 268.5 44.5 268.5 44.5 44.5 44.5 44.5 44.5 44.5 44.5 4		
11 11 11 11 11 11 11 11 11 11 11 11 11	20 21 22 23	24 25 27 28	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 0 4 2 6 4 7

### ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence:Rana (THER INFORMATION: catesbelana ribonuclease with Met at position 1, OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant COTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
                   Sequence 21, Application US/09948391A
; Sequence 21, Application US/09948391A
; Publication No. US2030027311A1
; GENERAL INPORMATION:
APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
US-09-948-391A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Gaps 0, Length 111; Indels 100.0%; Score 605; DB 10; 100.0%; Pred. No. 7.5e-61; ive 0; Mismatches 0; Query Match
Best Local Similarity 100.1
Matches 111; Conservative

0;

1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

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1 MONWATFOOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
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APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUWTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1996
CLASSIFICATION NUMBER: US 60/011,800
FILING DATE: 19-FEB-1996
APPLICATION NUMBER: US 60/011,800
FILING DATE: 19-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 015280-244100US
TELECHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGURL APPLICATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGURL APPLICATION:
TYPE: Amino acids
TYPE: Anino acids
TYPE: Trainey more representation.
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Search completed: May 7, 2004, 21:40:46 Job time: 12.8756 secs

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64 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
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                                                                                                                                                                                                 APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/875,811
FILING DATE: 19-FBE-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%; Score 273.5; DB 3;
48.6%; Pred. No. 3.7e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
                                                                                                                               Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 amino acids
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                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                         California
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Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-875-811-59
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                                                                                                                      US-08-875-811-63
                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                               RESULT 14
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                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                     60 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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45.2%; Score 273.5; DB 3; Length 112;
Best Local Similarity 48.2%; Pred. No. 3.1e-24;
Matches 54; Conservative 16; Mismatches 33; Indels 9.
                                                                                 Length 104;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                             Query Match 45.2%; Score 273.5; DB 4; Best Local Similarity 48.6%; Pred. No. 2.8e-24; Matches 54; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 112 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-875-811-32
                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-08-875-811-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                             ; MODECODE 1:
US-09-095-429-1
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2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: You-was and ani, Veena
APPLICANT: Worknesser
APPLICANT: Boix, Ester
TITLE OF INVENTION: A mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A llows Production by Recombinant Methods
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VLSTIRFQLNTCTRISITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                  45.2%; Score 273.5; DB 4;
48.6%; Pred. No. 2.8e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Townsend and Townsend and Crew
: One Market Plaza, Steuart Street Tower
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
                                                                    15280-267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 1528(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REPERENCE/DOCKET NUMBER: 152
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5643
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 48.6%;
                                                                                                                                                                                          104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94105-1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                   LENGIH:
                                                                                                                                                                                                                                                                                      US-08-626-288-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                       US-09-687-748-2
Sequence 2, Application US/09687748
Sequence 2, Application US/09687748
Sequence 2, Application US/09687748
Sequence 3, Application US/09687748
GENERAL INFORMATION:
TITLE OF INVESTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
TITLE OF INVESTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTHER OF SEQ ID NOS: 8
1 QDWLIFQKKHIINTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ONWAIFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ÓDMLÍFORKHITNÍRDVDCDNILSTNLF---HCKDKNIFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                        VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
                                                                  FEATURE:

OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at

OTHER INFORMATION: position 72
US-09-687-748-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 110
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APPLICANT: Vasandani, Veena
APPLICANT: Wa. Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.2%; Score 273.5; DB 4;
Best Local Similarity 49.5%; Pred. No. 2.8e-24;
Matches 55; Conservative 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOUR: IEM PC compatible
COMPOUR: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
STATE: California
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Patent No. 6649392
GENERAL INFORMATION:
APPLICANT: Youle, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 104
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US-08-626-288-1
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linear

TOPOLOGY:

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48.6%; Pred. No. 2.8e-24;
iive 16; Mismatches 32; Indels
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Patent No. 6423515
                                                                                                                                                                                                                                                  Sequence 2, Application US/09394268 Patent No. 6175003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
                    54; Conservative
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; ORGANISM: Rana pipiens
US-09-687-748-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 54; Conserv
   Similarity
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   Best Local
Matches 5
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Patent No. 617503

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: WAKING THEM
FILE REFERENCE: 5013
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEDWLTFOKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 275.5; DB 3; Length 358; Pred, No. 7.5e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels
                    FITLE OF INVENTION: Recombinant Ribonuclease Proteins NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 7435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 273.5;
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
       Wlodawer, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                      USA
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US-09-394-268-1
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                                                                                                                                                    COUNTRY:
       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: SAXMILLO.

PAPLICANT: SAXMILLO.

TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES FILE REFERENCE: 5013 US 01.

CURRENT APPLICATION NUMBER: US/09/687,748

CURRENT FILING DATE: 2000-10-14

PRIOR FILING DATE: 109/394,268

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

LENGTH: 104
4;
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                                                         2 ONWATFOOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                2 QNWATFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKALCTGVI-NLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: NUCLEIC ACIDS
FITLE OF INVENTION: MAKING THEM
FITLE REPRENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Gaps
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                                                                                                                                                                                                         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%; Score 273.5; DB 3; Length 104; llarity 49.5%; Pred. No. 2.8e-24; Conservative 15; Mismatches 32; Indels 9;
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DEVELOPMENTAL STAGE: Oocyte

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1 MQNWATFQQXHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL
    59 NVLSTTRFQLNTCTRTSITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRC 110
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Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susamna M.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcader Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.5%; Score 275.5; DB 3; Length 348.2%; Pred. No. 7.4e-24; live 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997

PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: FAZIS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET UNBER: 011
TELECOMMUNICATION:
TELECOMMUNICATION: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rybak, Susanna M.
Newton, Dianne L.
Boque, Lluis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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APPLICANT:
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                                                                                                                                      2 ONWAIFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                    1 MQNWATFQQKHINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
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                                                                                                         Gaps
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ف
                                                              Length 104;
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45.5%; Score 275.5; DB 3; Length 105;
Best Local Similarity 48.2%; Pred. No. 1.7e-24;
Matches 54; Conservative 17; Mismatches 32; Indels 9
                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
IITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend and Crew LLP
                                                      ch 46.4%; Score 280.5; DB 1 Similarity 48.6%; Pred. No. 4.4e-25; 54; Conservative 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTREET: TWO Embarcadero Center, Eighth F
STREET: Two Embarcadero Center, Eighth F
STATE: California
CUMATY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAWE: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015280-244100US
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Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 0152
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                             Best Local Similarity
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US-08-467-955-2
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                                                        Query Match
                                                                                               Matches
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4;

9; Gaps

Length 355;

28

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ORGANISM: Rana pipiens
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-875-811-8
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                                                                                                                                                                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08875811
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
; APPLICANT: Woldawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
INUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TROPPY disk
COMPUTER: IBM PC compatible
COMPUTER: DetentIn Release #1.0, Version #1.30
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-199
FILING DATE: 19-FEB-199
FILING DATE: 19-FEB-199
FILING DATE: 19-FEB-199
FILING DATE: 19-FEB-199
FILING DATE: 31-FEB-199
FILING DATE: 41-739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0300
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LEMETH AND ASSET INSTANCES:
LEMETH AND ASSET INSTANCES:
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LEMETH
                                                                                                                                                                                                                                         /note= "Frog Lectin from Rana catesbeiana"
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96.3%; Score 582.5; DB 2;
Best Local Similarity 96.4%; Pred. No. 5.9e-60;
Matches 107; Conservative 3; Mismatches 0;
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amino acid
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                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                  LOCATION: 1..111
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                               NAME/KEY: Protein LOCATION: 1..111
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                                                                                                                                                                                                                                                                                                                                   US-08-891-848-12
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US-08-875-811-8
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2 QNWAIFQQKHIINTFII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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US-08-467-955-2

US-08-467-955-2

Sequence 2, Application US/08467955

Patent No. 5728805

Patent No. 5728805

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANT: Ardelt Ph.D, Wojciech J.

APPLICANTON: PHARMACEUTICALS AND METHOD FOR MAKING THEM

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ASTRET: P.O. Box E

CONTRY: Short Hills

STATE: New Jersey

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: Datentin Release #1.24

CURRENT APPLICATION DATE:

PILING APPLICATION DATE:

APPLICATION DATE:

PILING DATE:

PILING DATE:

APPLICANTON DATE:

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APPLICANTON DATE:

APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSTIRFQLNTCIRTSITPRPCPYSSRIBINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                        Score 582.5; DB 3; Length 111;
Pred. No. 5.9e-60;
3; Mismatches 0; Indels 1;
/note= "Frog Lectin from Rana catesbeiana"
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDHER: US 07/179,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/814,332
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FBB-1992
PRIOR APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5007 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5
                                                                                                                                                                         96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 amino acids
                                                                                                                                                                                  Query Match
Best Local Similarity 96.4'
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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7, 2004, 21:28:45; Search time 12.8756 Seconds (without alignments) 445.066 Million cell updates/sec
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605
1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                 Copyright
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Perfect score:
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Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 12, Appli Sequence 2, Appli Sequence 39, Appli Sequence 41, Appl Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 32, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 65, Appli Sequence 65, Appli Sequence 66, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 67, Appli Sequence 55, Appli Sequence 55, Appli Sequence 55, Appli Sequence 55, Appli Sequence 55, Appli Sequence 55, Appli Appli Appli Appli Appli Appli Appli Description Sequence Sequence Sequence Sequence Sequence US-08-891-848-12 US-08-875-811-8 US-08-875-811-31 US-08-875-811-41 US-08-875-811-41 US-08-875-811-51 US-09-394-268-1 US-09-687-748-1 US-09-687-748-1 US-09-687-748-1 US-09-687-748-1 US-09-687-748-1 US-08-875-811-32 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-64 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-67 US-08-875-811-87 US-08-875-811-87 US-08-875-811-87 US-08-875-811-87 SUMMARIES Query Match Length DB 5 273 . 5 273 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 . 5 277 Result No. 

Sequence

Sequence 1, Appli	Segmence 1 Apply	Semiconor 1, Appril	+ (		Sequence 28, Appl		Sequence 24, Appl	Semience 45	7 6			, ,	1	Sednence 3, Appli	Sequence 47, Appl	Segmence 2 April :		7 / 7	Sequence 4, Appli		TIDDE 7 PERCE	Sequence 3, Appli
3 US-08-875-811-1	4 US-09-071-672-1	4 US-09-986-119-1	3 US-08-875-811-26	3 175-08-875-811-26	3 TIC-00 07E 011 20	2 TE 00 07F 011 01	57-TT9-C/0-07-C	3 US-08-875-811-45	3 US-08-875-811-53	00 110 00 00 011 0	02-118-6/8-90-60 6	3 US-08-875-811-22	3 715-09-223-118-3	2 TTO 00 021 42	3 US-UB-8/5-8II-4/	3 US-09-223-118-2	3 US-09-223-118-1	2 OFF CCC OC DIT C	5 03-03-773-TT8-4	3 US-08-875-811-2	c cr2 170-00-211 4	F-7/9-T/0-60-50 F
104	104	104	105	106	107	101	0 1	358	365	107	7	111	114	360	0 .	114	114	114	# 7 7	83	8	3
44.4	44.4	44.4	44.4	44.4	44	44		40.1	43.7	40.7		38.9	38.3	3.7 R		20.3	36.7	36 5		33.4	33.4	· )
268.5	268.5	268.5	268.5	268.5	268.5	267.5	364 5	0.407	264.5	246.5		435.5	232	228.5	200	777	222	221	1 0	707	202	
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ALIGNMENTS

389414

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	## PPLICATION NUMBER: US 08/014,082   FILING DATE: 04-FEB-1993   PRIOR APPLICATION DATA:   APPLICATION NUMBER: US 07/779,195   FILING DATE: 22-OCT-1991   PRIOR APPLICATION NUMBER: US 07/779,195   PRIOR APPLICATION NUMBER: US 07/510,696   ATTORNEY/AGENT INFORMATION:   APPLICATION NUMBER: US 07/510,696   ATTORNEY/AGENT INFORMATION:   NAME: Weber: Ellen Lauver:   REGISTRATION NUMBER: 32,762   TELECOMMUNICATION INFORMATION:   TELEPHONE: (415) 576-0200   INFORMATION FOR SEQ ID NO: 12:   SEQUENCE CHARACTERISTICS:   CENTRAL OF SEQ ID NO: 12:   SEQUENCE CHARACTERISTICS:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12:   CENTRAL OF SEQ ID NO: 12: 12: 12: 12: 12: 12: 12: 12: 12: 12
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New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                       'note= "Met not found in wild type RaPLR1"
                                                        /note= "Wild type Gln replaced with Ser"
                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                       Location/Qualifiers
                                                                                                                                                                                                                          Claim 34; Page 61; 71pp; English
                                                                                                         99WO-US006641.
                                                                                                                        98US-0079751P.
                                                                                                                                                          Rybak SM, Newton DL;
                                                                                                                                                                         1999-610847/52.
                                                                                                                                                                                                                                                                                                                             autoimmune diseases
                                                                                                                                                                         WPI; 1999-610847
N-PSDB; AAZ08129
                                Misc-difference
                                                Misc-difference
Rana pipiens.
                                                                                                         26-MAR-1999;
                                                                        WO9950398-A2
                                                                                         07-0CT-1999
        Synthetic
```

The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form 45.9%; Score 277.5; DB 2; Length 105; 48.2%; Pred. No. 1.9e-23; Arive 16; Mismatches 33; Indels 9: Query Match Best Local Similarity Sequence 105 AA;

1 MONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NL 58 Gaps 59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110 6 54; Conservative Matches g ò

26

AAY28879 standard; protein; 127 AA 25-JAN-2000 AAY28879 RESULT 15 

Search completed: May 7, 2004, 21:38:29

Job time : 47.3489 secs

Rana pipiens Clone 5alb ribonuclease.

(first entry)

Rana pipiens ribonuclease Clone Salb, RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moietry; CD22; cancerous B cell; onconase; Kaposi's Sarcona; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein; autoimmune disease

Rana pipiens

```
The present sequence is a Rana pipiens Clone Salb ribonuclease (RaPLRI). It is encoded by Clone Salb cDNA obtained from Rana pipiens liver mRNA residues II, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by becteria. The soluble expression of ribonucleases allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 VLSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENOYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VLITSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.9%; Score 277.5; DB 2; Length 127;
48.6%; Pred. No. 2.4e-23;
cive 16; Mismatches 32; Indels 9;
                                                                                              /label= Rana pipiens Clone 5alb_ribonuclease
        1. 23
/label= Signal_peptide
/note= "Putative"
24. 107
                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 69; 71pp; English.
                                                                                                                                                                                                   99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Conservative
                                                                                                                                                                                                                                                                                                    Newton DL;
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610847/52.
N-PSDB; AAZ08136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 127 AA;
                                                                                                                               WO9950398-A2
                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                   27-MAR-1998;
                                                                                                                                                                 07-0CT-1999
                                                                                                                                                                                                                                                                                                      Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases
               Key
Peptide
                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Rana pipiens liver ribonuclease (RaPLR1)

25-JAN-2000 (first entry)

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This sequence represents recombinant frog Onconase. Onconase has ribonuclease and anti-tumour activity. The CDNA was produced via PCR cusing primers AA219769 of two synthetic DNAS whose sequences cancoded most of the N-terminal or the C-terminal amino acids of mature or acids (minus the initial methionine) or the C-terminal 51 amino acids, and were ligated in frame at an Nrul site. The CDNA was then caids, and were ligated in frame at an Nrul site. The CDNA was then caids, and were ligated in Frame at an Nrul site. The CDNA was then caids, and were ligated to the CDNA. After expression in E coli, the recombinant comparable of the CDNA. After expression in E coli, the recombinant control of the CDNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli, the recombinant control of the DNA. After expression in E coli of the DNA. After expression is a colidated as a result of potent inhibition of protein synthesis by a manualian placental ribonuclease inhibitor, which may explain its manualian placental ribonuclease inhibitor, which may explain its continuity against a variety of solid tumours e.g. colon or pancreatic cancers, and can be used alone or in combination with other anti-tumour can be conjugated to a marker which targets it to a specific cell type
                                                                                                                          Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A new recombinant Onconase used to treat, e.g. colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                     Leung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                      99WO-US004252.
                                                                                                                                                                                                                                                                                                                                              98US-0077557P.
                                        (first entry)
                                                                                    Recombinant frog Onconase.
                                                                                                                                                                                                                                                                                                                                                                                                                              Goldenberg DM, Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                      (IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-551416/46.
N-PSDB; AAZ19767.
                                                                                                                                                                       Rana pipiens
                                                                                                                                                                                                                 WO9946389-A1
                                                                                                                                                                                                                                                                                                 11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                            11-MAR-1998;
                                          01-DEC-1999
                                                                                                                                                                                                                                                         16-SEP-1999.
  AAY39400;
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1 MONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NL 58
                                                       Gaps
                                                         9.
                              DB 2; Length 105;
                                                       Indels
                         ; Score 278.5; DB 2;
; Pred. No. 1.5e-23;
16; Mismatches 32;
                           46.0%;
                                                   55; Conservative
                                        Local Similarity
Sequence 105 AA;
                         Query Match
                                        Best Loca
Matches
                                                                              δ
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4

9; Gaps

Length 104; Indels

DB 2; 32;

45.9%; Score 277.5; DB 2 48.6%; Pred. No. 1.9e-23; tive 16; Mismatches 32

54; Conservative

Similarity

Query Match Local Matches 59 56

2 QNWATPQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN

> g à q

60 VLSTIRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110 

> 59 NVLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110

> > g à QQ

RESULT 13 AAY28865

AAY28865 standard; protein; 104 AA.

Recombinant Met (-1) Rana pipiens ribonuclease Glniser; RaplR1; CD22; Covalently bound; LL2 antibody; ligand binding moiety; cancerous B ce. Raposi: s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease; RNase.

Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.

(first entry)

25-JAN-2000

AAY28871;

AAY28871 standard; protein; 105 AA.

RESULT 14

AAY2887

AAY28865; HXXX

```
The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein. Carboxy terminal end of RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer
                                                                   Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 55; 71pp; English.
                                                                                                                                                                                                                                                                       99WO-US006641.
                                                                                                                                                                                                                                                                                                           98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104 AA;
                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                               Rana pipiens
                                                                                                                                                                                                 WO9950398-A2
                                                                                                                                                                                                                                                                                                         27-MAR-1998;
                                                                                                                                                                                                                                   07-0CT-1999.
                                                                                                                                                                                                                                                                                                                                                                                Rybak SM,
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g à

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AAY28866 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
AAY28866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW1824, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens ocytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
                                                                              1 MODWLTFOKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                        Gaps
                                                                                                  59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                              VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.4%; Score 280.5; DB 2; Length 104; 48.6%; Pred. No. 8.7e-24; ive 17; Mismatches 31; Indels 9
                    Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                       Indels
                    DB 2;
                                        32;
                    ; Score 282.5; DB 2
; Pred. No. 5.2e-24;
16; Mismatches 32
                                                                                                                                                                                                                                   Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                      Fumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 28; 45pp; English
                                                                                                                                                                       AAW06544 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                        95US-00467955.
                                                                                                                                                                                                                                                                                                                                     96WO-US008304.
                    46.78;
                               49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                             (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104 AA;
 Sequence 105 AA;
                                                                                                                                                                                                                                                                           Rana pipiens
                                                                                                                                                                                                                                                                                              WO9639428-A1
                                                                                                                                                                                                                                                                                                                                     03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                  12-DEC-1996
                                        52;
                                                                                                                                                                                                              22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                 Ardelt WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                    Query Match
Best Local 8
                                                                                                                                                                                           AAW06544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                        Matches
                                                                                                                                                    RESULT 10
                                                                                                                                                               AAW06544
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11

RESULT

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                                                                                                                                                             Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cyctoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Met replaced with Leu"
                                                                                                          Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%; Score 279.5; DB 2 49.5%; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY39400 standard; protein; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 34; Page 56; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0079751P.
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                    autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ08125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                            Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1998;
                                                     25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rybak SM,
AAY28866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
AAY39400
ID AAY39
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1;
                                                                                                                                                                                                       ONWATFQOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
                                                                                                                                                                                                                                        The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi, s sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6, RaPLRI; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
(Rana catesbeiana) lectin used to describe the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                              LSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                               1;
                                                                                                              Length 111;
                                                                                                                                                                                                                                                                                                                                              'note= "Met not found in wild type RaPLR1"
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                         0;
                                                                                                           DB 2;
                                                                                                         Score 582.5; DB 2
Pred. No. 6.3e-58;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28869 standard; protein; 105
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                                                                                                         96.3%;
96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US006641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                 Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-610847/52.
                                                                                                                            Local Similarity
                                                   Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ08127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9950398-A2
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                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY28869;
                                                                                                      Query Match
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4;
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                                                                                                                                1 MONWAIFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                       cell;
ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cel. Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                             59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                            9;
                                                                             Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Met not found in wild type RaPLR1"
                                                                                                         Indels
                                                                          Score 284.5; DB 2;
Pred. No. 3.1e-24;
                                                               47.0%; Scc. No. 5...
50.0%; Pred. No. 5...
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 34; Page 57; 71pp; English.
                                                                                                                                                                                                                                                                                                AAY28867 standard; protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Met(-1) RaPLR1.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                      56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-610847/52.
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ08126
                                             Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9950398-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rybak SM,
                                                                                                                                                                                                                                                                                                                               AAY28867;
                                                                                                      Matches
                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                  AAY28867
 SXSS
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0; 62

Gaps

· 0

Length 110; 0; Indels

Score 591; DB 2; Pred. No. 6.8e-59;

97.7%;

2; Mismatches

Conservative

107;

a

0

0; Gaps

Length 111; Indels 9

Similarity

Query Match Best Local S Matches 3 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS

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The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with GlnISer. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                             1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                              1 MONWATFOOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                    LSTTRFOLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild type Gln replaced with Ser"
                                                             Score 596; DB 2; D Pred. No. 1.9e-59; 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 67; 71pp; English.
                                                                                                                                                                                                                                                                                                                    AAY28877 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0079751P
                                                             y Match 98.5%;
Local Similarity 97.3%;
hes 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
autoimmune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                 Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                     AAY28877;
                                                                  Query Match
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                                                                                  Best Loca
Matches
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autoimmune diseases

Sequence 110 AA;

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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a specific agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (eff'y)-1, Especial-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster.

CYCOMEGALOVIUS)) and cells infected with parasites (such as the malaria cyromegalovirus)) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
                                                                                                                                                                                                                                                                                                                                                                                         heavy chain, cell surface marker; treatment; tumor; viral infection; parasite infection; mmune dysfunctional cell; autoimune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; I-cell; graft-versus-host disease; bullfrog; lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antly fused pancreatic RNase-targeting proteins useful for tumors, infections, immune or autoimmune disorders and as
                                                                                                                                                                                                                                                                                                                                                                          Cytotoxic, RNase, ribonuclease, pancreatic, antibody; light chain;
                                                                               TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                            63 TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicholls PJ, Youle RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                          AAY33321 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 19; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00510696.
                                                                                                                                                                                                                                                                                                                                   Frog lectin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00891848.
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93US-00125462
                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana catesbeiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1997;
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22-OCT-1991;
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22-SEP-1993;
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                                                                                                                                                                 RESULT
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cytotoxic fusion proteins. They can be used for treatment of cancer and

autoimmune diseases

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Sequence 110 AA;

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end of recombinant RacOR1 has a covalently bound ligand binding moiety, which can be a Li2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methiconine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of tibonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                QNWATFQQXHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
                                                                                                                                                                                                                                     ONWATFQCKHILINTFILCHTILDNNIYIVGGCKRVNTFILSSATTVKAICTGVININVL
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
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                                                                                                                                                                                                                                                                 STIRFQLNICTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                               Score 600; DB 2; Length 110;
                                                                                                                                                                                         Indels
                                                                                                                                                                                          0;
                                                                                                                                                                            6.5e-60;
                                                                                                                                                                          Local Similarity 100.0%; Pred. No. 6.5
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                                                                                                                                                                                                                                                                                                                                                            AAY28872 standard; protein; 110 AA
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                                                                                                                                                                99.2%;
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                                                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana catesbeiana
                                                                                                                                   Sequence 110 AA;
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1, covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Raposi's sarcoma; human chorionic gonadotrophin; hGG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease.
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                                                                                     QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                2 ONWAIFQORHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                   STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                    ..
                                                                                                                                  STIRFQLNICTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP
   Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Met not found in wild type RaCOR1"
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
                                  .,0
Score 596; DB 2;
Pred. No. 1.8e-59;
                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                               AAY28878 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Page 68; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant ribonucleases,
98.5%;
98.2%;
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                                                                                                                                                                                                                                                                                                                 (first entry)
                               Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-610847/52.
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rana catesbeiana.
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                                                                                                                                                                                                                                                                                  AAY28878;
Query Match
Best Local 9
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The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RaCOR1 has a covalently bound ligand binding moiety, which can be a LiZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma edlls. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form

for

New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.

WPI; 1999-610847/52.

N-PSDB; AAZ08130.

Claim 22; Page 62; 71pp; English.

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ribonuclease (RaCCR1) protein with Met at position 1 attached to a (His)6 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCCR1 has a covalently bound ligand binding moiery, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RacOR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
                                                                                                                                                                                                                                                                                                         1 MQNWATFQQXHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                MONWATEQOKHILINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                        LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                         sequence is a recombinant Rana catesbelana oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Met not found in wild type RaCOR1"
                                                                                                                                                                                                                                              Score 605; DB 2;
Pred. No. 1.8e-60;
                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY28873 standard; protein; 111
                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNase; autoimmune disease
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newton DL;
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                                                                                                                                                                                                                                                              Local Similarity
les 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catesbeiana
                                                                                                                                                                                                                   Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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             end of recombinant RacOR1 has a covalently bound ligand binding modety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorizonic gonadotrophin (HCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; Racorl Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target cells, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a recombinant Rana catesbeiana occyte ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
protein with Met at position 1. Carboxy terminal
                                                                                                                                                                                                                                                        1 MONWATFOOKHIINTPIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                61 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                    61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                            .,
                                                                                                                                                                                              2; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant ribonucleases, used for killing target cel
treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Met replaced with
                                                                                                                                                                                                Score 601; DB 2;
Pred. No. 5e-60;
                                                                                                                                                                                                                              2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28874 standard; protein; 110
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                                                                                                                                                                                                y Match
Local Similarity 98.2%;
hes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Newton DL;
         (RaCOR1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-610847/52.
                                                                                                                                           autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana catesbeiana.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ08132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                       Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1998;
          ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28874;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                      Best Loca
Matches
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          88888888888888
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for

The present sequence is a recombinant Rana catesbelana oocyte

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0; Gaps

Indels

Length 111;

OM protein - protein search, using sw model

7, 2004, 21:25:55 ; Search time 47.3489 Seconds (without alignments) 662.376 Million cell updates/sec May Run on:

US-09-961-400-21

Perfect score: Title:

605 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB &

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp1980s:*

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* 

geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description											Aaw06544 Antitumou	Aav28866 Recombina				ž,	Kar	Α.		Α.	Aaw30301 Recombina		0		o 1	151 / NO1	SII8 K.	Aaw35134 R. pipien
SUMMARIES	ID	AAY28876	AAY28873	AAV28874	AAY28872	AAY28878	AAV28877	AAV33221	AAV20050	C0002177	/ 00071GG	AAWU6544	AAY28866	AAY39400	AAY28865	AAY28871	AAV28879		ANICOLEGO	AMMOSICO	OCTOPING COLUMN	AAM30301	AAB31667	AAB31666	ABG32650	ABG31617	AAW35118	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AAW35134
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æ	Query	100.0	99.3	99.2	98.5	98.5	97.7	96.3	47.0	46.7	v	٥ ١	46.7	ġ	45.9	45.9	45.9		Ľ	) LC			•	•	45.2	45.2		u	·
	Score	605	109	009	296	296	591	582.5	284.5					2.8.5	•	277.5		275.5		275.5			٠	٠		273.5	273.5		
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Aaw35135 R. pipien	굓 다	Adwooley K. pipien	Ļρ	Aaw30300 Decembing									Adysssz Frog onco	χ (	<b>.</b>	Aaw35117 R. pipien	Aaw35115 R. pipien	ρ	α,
AAW35135	AAW35133 AAW35129	AAW35132	AAW35126	AAW30302	AAY28870	AAR12344	AAR47303	AAW00736	AAW14065	AAWO6543	AAW88233	AAY3322	AAWAS116	AAW35122	111111111111111111111111111111111111111	/ TTCCHOR	AAW35115	AAW35127	AAW35131
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254	3 55 3 55 3 55 3 55 3 55 3 55 3 55 3 55	366	379	104	104	104	104	104	104	104	104	104	105	106	107	) (	105	358	365
45.2	45.2	45.2	45.2	45.0	45.0	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.4	44.4	44 4		7 1	43.7	43.7
273.5	273.5	273.5	273.5	272.5	272.5	270.5	270.5	270.5	270.5	270.5	270.5	270.5	268.5	268.5	268.5	3 636		264.5	264.5
26	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43		44	45

#### ALIGNMENTS

RESULT 1 AAY28876

AAY28876 standard; protein; 111 AA.  XX XX XX XX XX XX XX XX XX XX XX XX X	
XXX XXX XXX XXX XXX XXX XXX XXX XXX XX	3

(His) 6; RaCOR1; I binding moiety; lotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.

Rana catesbeiana. Synthetic.

Location/Qualifiers Misc-difference 

note= "(His)6 histidine tag attached to N-terminal Met" 'note= "Met not found in wild type RaCOR1" Misc-difference

note= "Wild type Met replaced with Leu" 58 /note= "Wild type Met replaced with Leu" Misc-difference 23 Misc-difference

WO9950398-A2

07-OCT-1999.

99WO-US006641 26-MAR-1999;

98US-0079751P. 27-MAR-1998; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Rybak SM, Newton DL;

1999-610847/52. WPI;

N-PSDB; AAZ08133.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 66; 71pp; English.

```
RA Beintema J.J.;

RT "Secretory ribonucless genes and pseudogenes in true ruminants.";

RT "Secretory ribonucless genes and pseudogenes in true ruminants.";

RG Gene 212:559-268(1998).

CC -1- STMILARITY: Belongs to the pancreatic ribonuclesse family.

-1- SIMILARITY: Belongs to the pancreatic ribonuclesse family.

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CC or send an email to license@ais-sib.ch).

CC or send an email to license@ais-sib.ch).

CR REMEL; Y11670; CAA7236B.1; -

DR HSSP; PRO0079; RRNO0794; RIBONUCLEASE.

DR FRINTS; RR000794; RIBONUCLEASE.

DR PRO0079; RNASE PC; 1.

DR PRONO79; RNASE PC; 1.

DR PRONO79; RNASE PC; 1.

DR SWART; SN00092; RNASE PC; 1.

CR DISULFID 40 95 BY SIMILARITY.

FT DISULFID 58 110 BY SIMILARITY.

FT DISULFID 65 72 BY SIMILARITY.

FT CARBOHYD 62 62 C2 N-LINKED (BY SIMILARITY).

FT CARBOHYD 133 133 0-LINKED (BY SIMILARITY).

SQ SEQUENCE 151 AA; 16819 MW; B95F757FFCSB233 CRC64;

QUELY MACCH 8: 36; CODSETVATIVE 18; Bred. NO. 2.2-06; BRET. Indels 23; Gaps 7;

MACCH 8: 36; CODSETVATIVE 18; Bred. NO. 2.2-06; BRET. Indels 23; Gaps 7;
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Search completed: May 7, 2004, 21:53:06 Job time : 5.55659 secs

105 G 105 | | 122 G 122

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[2]
SEQUENCE OF 31-114 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cervidae;
                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNBR_AXIPR
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                                                                                                                                                                                                                                                                                                                                                 6 FOOKHIINTPI----ICNTILDNNIYIVGGOCKRVNTFIISSATTVKAIC---TGVINL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
                                                     13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96139017; PubMed=8587129;
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant
  Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                      20.6%; Score 123.5; DB 1; Length 123; 29.6%; Pred. No. 1.8e-06; tive 20; Mismatches 43; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                58 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTEINYICVKCENQYPVH 102
                                                                                                                                                                                                                           CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                 33 N-LINKED (GLCNAC. . .).
14522 MW; B703B9839919FD2F CRC64;
                                                                                                                                                                                                   Hydrolase, Nuclease, Endonuclease, Anglogenesis,
Protein synthesis inhibitor; Glycoprotein;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                      GIRCA SILL.

RNBR GIRCA SILL.

Q29542; Q20533;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                  SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                            PYRROLIDONE
                                                                                                                                                     Interpro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe PC; 1.
PROSITE; PS00127; RNASE PANNREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giraffa camelopardalis (Giraffe).
                                         TISSUE=Milk, and Serum;
MEDLINE=97409980; PubMed=9266695;
                                                                                                                                                                                                                                   BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            species.";
J. Mol. Evol. 41:850-858(1995).
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                   12
39
113
80
91
           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giraffidae; Giraffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
   Eutheria;
                                                                                                                                                                                                                                                                                           123 AA;
                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                HSSP; P10152; 1AGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9894;
                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                   ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                           DISULFID
            Bovidae;
                                                                                                                                                                                                                                                                                   CARBOHYD
                                  SEQUENCE
                                                                                                                                                                                                                             MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                       RNBR GIRCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 NVL-----STIRFQLNTCIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHFA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ATFOOKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKFRRQHMDSGSSSSSNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLADVKAVCS---QK 61
     Brenkelman H.J., Beintema J.J., Confalone B., Costanzo C., Sasso M.P., Carsana A., Palmieri M., Furia A.; Sequences related to the ox pancreatic ribonuclease coding region in the genomic DNA of mammalian species.";
J. Mol. Evol. 37:29-35(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Nuclease; Endonclease; Glycoprotein.
ACT SITE
DISTURED
26 84 BY SIMILARITY.
DISTURED
40 95 BY SIMILARITY.
DISTURED
58 110 BY SIMILARITY.
DISTURED
65 72 BY SIMILARITY.
CARBOHYD
62 62 N-LINKED (BY SIMILARITY).
CARROHYD
129 129 0-LINKED (BY SIMILARITY).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                               -:- SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73745EFE9079591F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1e-06;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.6%; Score 123.5; 29.8%; Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                 J. Mol. Evol. 37:29-35(1993).
-!- SUBCELLULAR LOCATION: Secreted.
MEDLINE=93367815; PubMed=8360916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 BY
84 BY
95 BY
110 BY
72 BY
62 N-
129 M'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00794; RIBONUCLEASE. ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S81743; AAB36137.1; -. EMBL; S65126; AAB27931.1; -. HSSP; P00656; ZRNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cervinae; Axis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA;
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129
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RNBR

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7;
                                                                             --STTRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHFA 104
                                                                                                     88 NITCKNGHPNCYQSKSTMSITDCREİGSSKYPNCAYKTSQKQKYİTVACEGNPYVPVHPD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                         4 ATFOOKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ONWATFOOKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'-
U-P
                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIACENNQPVHF
        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ribonuclease.";

Eur. J. Biochem. 219:641-646(1994).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELIGUAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

MOD RES

1 1 PYRROLIDONE CARBOXYLIC ACID.

DISULED 25 80 BY SIMILARITY.

DISULED 57 106 BY SIMILARITY.

ACT_SITE 10 10 BY SIMILARITY.

ACT_SITE 10 10 BY SIMILARITY.

ACT_SITE 11 11 BY SIMILARITY.

ACT_SITE 11 11 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                   Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguani
                                                                                                                                                                                                                                                                                                                                                                                                                Zhao W., Beintema J.J., Hofsteenge J.; "The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
Iguana iguana (Common iguana).
     43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6072FB5B7B15BD5A CRC64;
                                                                                                                                                                                                                                                                                                                     Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 127.5; DB ]
Pred. No. 6.5e-07;
                                                                                                                                                                                                                                 119 AA.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; PD000535; RNASeA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94139745; PubMed=8307028;
    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P00656, 1LSQ.
InterPro; IPR001427; RNaseA.
Pfam; PF00704; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%;
  Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S41111; S41111.
HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                             58 NVL----
                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Pancreas;
                                                                                                                                                            148
                                                                                                                                  105 G 105
37;
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                                                                                                                                                                                                                            IGUIG
                                                    32
                                                                                                                                                           148
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SEQUENCE
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Best Local
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P80287
                                                                                                                                                                                                             RNP_IGUIG
ID RNP_I
Matches
                                                                                                                                                                                               RESULT 11
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RESULT 12

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 NVL-----STTRPQLNTCTRTSITPRP-CPYSSRIEINYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NITCKNGQPNCYQSNSTWNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ATFQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL
                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Ribonuclease, brain (BC 3.1.27.-) (BRB).
Capreolus capreolus (Roe deer).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetariiodactyla; Ruminantia; Pecora; Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interection Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter Promoter 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124.5; DB 1
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
            151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AA
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            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98278842; Pubmed=9611269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y11673; CAA72371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%;
28.6%;
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            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beintema J.J
CAPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANG2 BOVIN
P80929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
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16-OCT-2001 (Rel. 40, Last annotation update) Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
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GlycoSuiteDB; P39873; --
InterPro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA; I.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X59767; CAA42439.1; -. EMBL; S81744; AAB36138.1; -. PIR; S20066; S20066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6%;
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159
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167
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67
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121
136
98
88
                                          taurus (Bovine).
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155
167 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
38
67
                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                              rissue=Brain;
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ACT_SITE
ACT_SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 FOROHMDPDSSSSNSSNYCNIAMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66
                                                                                                                                                                                                      REVISION TO 2. Wherever a desire we willing G.W., Beintema J.J., Wherever a desirema J.J., Wherever a desirema by the weak of porcine parcreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence."; FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 FQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NGQINCYQSNSTMHIIDCRQIGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 245:654-661(1970).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside in phosphates and 3'-phosphooligonucleotides ending in C-P or With 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; A92071; NRPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6%; Score 129.5; DB 1; Length 124; 30.7%; Pred. No. 4.1e-07; ive 20; Mismatches 42; Indels 17;
                                                                                                                                       Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653(1970).
                                                                                                                                                                                                                                                                                                            Phelan J.J., Hirs C.H.W.; "The primary structure of porcine pancreatic ribonuclease. 3. disulfide bonds.";
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LINKED (GLCNAC. . .).
OAC28CDE14111845 CRC64;
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N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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InterPro; IPRO01427; RNaseA.
Pfam; PF00074; rnaseA, 1.
Prons; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pro; 1.
PROSIL7; RNSSE PANCEATIC; 1.
HYGOLASE; NUCLEASE; Endonuclease; Glycoprotein.
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(Rel. 31, Last sequence update)
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MEDLINE=70104198; PubMed=4904878;
                                                                                                                          MEDLINE=70104197; PubMed=5460946;
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                                             Sus scrofa (Pig).
                                                                                   NCBI_TaxID=9823
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01-FEB-1995
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                                                                                                                                                         [1] SEQUENCE FROM N.A. MDMed=1754384; Cosi C., Sorrentino S., MEDLINE=92093604; PubMed=1754384; Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S., Viola M., Palmieri M., Russo E., Furia A.; Wolecular cloning of the gene encoding the bovine brain ribonuclease "Molecular cloning of the gene encoding of the brain."; and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474(1991).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Boyidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89214015; PubMed-3243767;
Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
Ohgi K., Irie M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 27-167 FROM N.A.
MEDIJNE=96139017; PubMed=8587129;
Onfalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Mol. Evol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of a ribonuclease from bovine brain."; J. Biochem. 104:939-945(1988).
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> S (IN REF. 2).
681CAAC3CC2FC459 CRC64;
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N-LINEED (GLCNAC...
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Mara S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzry D.M., Sodergren B.J., Lu K., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blackelley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1162:177-186 (1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothalial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothalial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenins: discernment of functionally important residues and regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                     TISSUE-Serum,
MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.,
"Characterization and sequencing of rabbit, pig and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SUBCELLULAR LOCATION: Secreted.
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MGD; MGI:88022; Ang.
InterPro; 1PR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U22516; AAA91366.1; -.
EMBL; BC055355; AAH55355.1; -.
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                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 L-----STTRFQLNTCTRISITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                       Emmens M., Welling G.W., Beintema J.J., "The amino acid sequence of pike-whale (lesser-rorgual) pancreatic
                                                                                                                                                                                                                                                    Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Endourcleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.

    I-TISSUE SPECIFICITY: Pancreas.
    SIMILARITY: Belongs to the pancreatic ribonuclease family.

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N-LINKED (GLCNAC. . .) (30%).
                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
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                                                                                                                                                     124
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=76277855; PubMed=962870;
                                                                          122 GFRHVVIACENGLPVHF 138
                                             87 ETNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 157:317-323(1976).
                                                                                                                                                                                                                                                                                             Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14125 MW;
                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9767
                                                                                                                                                                                                                                                                                                                                                                                                    ribonuclease.";
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DB 1; Length 145;

22.8%; Score 136.5; DB 1 40.3%; Pred. No. 8.6e-08;

28;

11; Mismatches

31; Conservative

Matches

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO THE FEFFE FEFFE SO DRAWER SO THE SOUTH STATES OF SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SOUTH SO
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129; TISSUE-Liver; MEDLINE=96079109; PubMed=8530072; Brown W.E., Nobile V., Subramanian V., Shapiro R.; Brown W.E., Nobile V., Subramanian V., Shapiro R.; "The mouse anglogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes."; Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                 Mol. Cell. Biol. 17:1503-1512(1997).

Mol. Cell. Biol. 17:1503-1512(1997).

-!- FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Angiolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amatch 25.8%; Score 154.5; DB 1; Length Local Similarity 43.6%; Pred. No. 9.9e-10; Length es 34; Conservative 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, DE9D3BC92F1D682C CRC64;
  developmentally regulated genes when expressed in NIH 3T3
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGIOGENIN-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANTEATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenin-related protein precursor. ANGRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : || : ||| : ||||
121 KDFRYIVIACEDGWPVHF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00794; RIBONUCLEASE. ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
16696 MW;
                                                                                                                                                                                                                                                                                                                    EMBL; U72672; AAC05794.1; -
HSSP; P10152; 1AGI.
MGD; MGI:1201793; Angl.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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145
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64
137
104
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137
50
63
145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                           fibroblasts."
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28-FEB-2003
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Q64438;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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MOD_RES
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNIRI-SKSRFQVTTCTHKGRSPRPPCRYRASK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CKRVNTFIISSATTVKAICTGV----INLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4e-09;
es 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29A6EB814429C4AD CRC64;
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Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AA.
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PRINTS; PRO0794; RIBONUCLEASE.
PRO0794; RIBONUCLEASE.
PRO07195; RNASE, 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Pyrrolidone carboxylic acid. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%; Score 149.5; 44.2%; Pred. No. 3.46
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9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : ||| : ||||
122 GFRYIIIGCENGWPVHF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16612 MW;
                                                                                                                                                                                                                                                                                                                                             MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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54;
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ACT_SITE
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DISULFID
DISULFID
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DISULFID
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ANG3 MOUS
      셤
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                                                                                                                                                                                                                                               1 ONWATFQOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                          2; Gaps
                                                              -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR, 3X0085; 3X0085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens occytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosimann S.C., Ardelt W., James M.N.G.;
"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";
J. Mol. Biol. 236:1141-1153(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens cocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 21, 20, Last annotation update)
0-30 protein (EC 3.1.27.-) (Onconase).
0-30 protein (Northern leopard frog).
0-30 protein Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rania.
                                                                                                                                                                                                                                                                                  VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                             MEDLINE=93066156; PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                Score 370; DB 1;
Pred. No. 4.7e-33;
                                                                                                                                                                                                                                                                                                                                                104 AA
                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                               Score 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=94166079; PubMed=8120892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91093131; PubMed=1985896;
Biochem. 106:729-735(1989).
                                                                                                                                                                                                              64.98;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-STRUCTURE MODELING.
                                                                                                                                                                                                   HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                             RN30 RANPI
P22069;
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                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                      -!- DEVELOPMENTAL STAGE: Barly embryos (up to four blastomere stage)
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; 10NC; 31-JAN-94.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin-3 precursor (EC 3.1.27.-) (Anglogenin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|:||:||:||
VLTTSEFYLSDC---NVTSRPCKYKIKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c;
MEDLINE=97184476; PubMed=9032278;
Fu X., Kamps M.P.;
"E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                             Pfam; PF00074; rnaseA; 1.
ProDom; PF00055; RNaseA; 1.
SMART; RN00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCEATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 273.5; DB 1; Pred. No. 1.1e-22; 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.6%;
                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                     10
941
947
970
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930
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948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       110
31
32
330
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87
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01-NOV-1997
28-FEB-2003
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4,

acid-binding lectin (EC 3.1.27.-).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONWAIFQOXHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
       as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and subsunIT: Monomer.
                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNAse Pc; 1.
PROSTE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endomuclease; Sialic acid; Lectin; 3D-structure;
Signal; Pyrrolidone carboxylic acid.
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                      -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
14762 MW; A7D62594F7D16F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  RIBONUCLEASE, OOCYTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 585.5; DB 1,
Pred. No. 3.6e-56;
2; Mismatches 0
                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                             EMBL; AF039104; AAD10702.1; -.
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                                                                                                                                                                                                                                                                                    InterPro; LENCON-1-1
Pfam; PP00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                      PDB; 1BC4; 28-OCT-98.
PDB; 1M07; 21-JAN-03.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  133
23
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73
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84
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                                                                                                                                                                                                                                             PIR; A27121; A27121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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SEQUENCE
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ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LECS RANJA
ID LECS RP
AC P18839;
DT 01-NOV-
DT 01-FEB-
DT 10-OCT-
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HELIX
TURN
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Last sequence update)
Last annotation update)

01-FEB-1994 10-OCT-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QNWAKEQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitta R., Katayama M., Matanabe H., Abe Y., Okazaki T., Ohgi M., Irie M., "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                        Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.; "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                                                                 J. Biochem. 108:139-143(1990).
-!- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but does not agglutinate non-transformed cells and erythrocytes.
-!- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kana catespelana (BULL 1709).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
         Rana japonica (Japanese reddish frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SWART; SM00092; RNASe Pc; 1.
PROSITIE; PS00127; RNASE PANCERATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.2%; Score 451; DB 1; 77.5%; Pred. No. 9e-42; ive 8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ribonuclease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90130374; PubMed=2613682;
                                                                                                 TISSUE=E99;
MEDLINE=91035319; PubMed=2229005;
                                                                                    SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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35
104
72
82
97
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HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8400;
                                                         NCBI TaxID=8402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _RNPL_RANCA
P14626;
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ACT_SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD RES
                                                                                                                                                                           eggs."
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OM protein - protein search, using sw model

7, 2004, 21:30:40 ; Search time 5.55659 Seconds (without alignments) 1030.796 Million cell updates/sec May Run on:

US-09-961-400-19 600 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	D11916 range sates	g rana	מומי		mis m	TINE SITE		bala	-	pog	iona				axis por	idoim		cerconit		מואס	P00686 macropus ru		anti			_	P00683 mus musculu	•	P00679 cavia porce	P10152 bos taurus	came	_	o homo s
SUMMARIES	ΩI	RNPO RANCA	LECS RANJA		RN30 RANPI	ANG3 MOUSE	ANGR_MOUSE	ANGI MOUSE	RNP BALAC	RNP_PIG	RNBR BOVIN	RNP_IGUIG	RNBR CAPCA	ANG2_BOVIN	RNBR_GIRCA	RNBR AXIPR	ANGI MIOTA	ANGI_SAISC	ANGI CERAE	ANGI PONPY	RNBR_SHEEP	RNP MACRU	ANGI_PIG	RNP_ANTAM	ANGI_AOTTR	ANGI_SAGOE	RNP_MYOCO	RNP_MOUSE	ANGI MACMU	RNPB_CAVPO	ANGI_BOVIN	RNP CAMDR	RNP HORSE	ANGI_HUMAN
	DB	4	Н	П	Н	Н	1	1	П	Н	П	Н	Н						П	Н	г	ч					Н.				1	٦	Н	Н
	Length	133	111	111	104	145	145	145	124	124	167	119	151	123	141	151	146	146	146	147	143	122	123	124	146	146	128	149	146	128	148	124	128	147
οķο	Query Match	97.6	75.2	61.7	Ŋ	'n.	4.	22.8	21.9	21.6	21.6	21.2	20.8	20.6	20.6	20.6	20.5	20.5	20.0	20.0	19.9	19.8	19.8	19.8	19.7	19.5					19.0			
		585.5	451	370	273.5	154.5	149.5	136.5	131.5	129.5	129.5	127.5	124.5	123.5	123.5	123.5	123	123	120	120	119.5	119	118.5	118.5	877	117	Η г	4.911	115	114.5	114	113.5	113.5	113
	Result No.	- T	2	m	4	S.	9	7	Φ.	ص	0 1	7	12	E I	<b>⊣</b> +	15	91	17	87,	1.9	20	21	7.7.7	23	4 1	25	9 10	770	20 00	67	30	31	32	33

Q8wme8 pan troglod	P1546/ DOS caurus P04059 proechimys	Q8wn64 papio hamad	P31347 oryctolagus	P00664 capreolus c P00662 giraffa cam	P24717 cricetulus P00657 bubalua bub	Q9wuv5 peromyscus
ANGI PANTR	RNP PROGU	ANGI PAPHA	ANGI_RABIT	RNP_GIRCA	RNP_CRILO RNP_BUBBU	RNP_PERLE
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147	128	146	125	124	130	148
18.8	18.8	18.2	18.2	18:1	18.1 17.9	17.9
113	112.5	109.5	109	108.5	108.5	107.5
3.4 5.4	36	8 6 6 6	40	4.4	4, 4, U 4,	45

### ALIGNMENTS

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---INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
                                                                                  89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQXQKHIIVACEGNPYVPVHF 145
                                                             60 L-----STTRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 103
 6 FOOKHI---
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pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
NyAlternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a A;Reference number: A91247; MUID:77188023; PMID:862624

A; Molecule type: protein A; Residues: 1-128 <VAN> A; Note: 64-Pro was also found

C;Superfamily: pancreatic ribonuclease C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 30.8%; Pred. No. 0.00024;
Matches 36; Conservative 15; Mismatches 43; Indels 23;

59 6 FOOKHI-----INTPLICNTILDNNIYIVGGOCKRVNTFIISSATTVKALCTGVINLNV

> Db 8

Search completed: May 7, 2004, 21:54:56 Job time: 10.9813 secs

angiogenin - pig

8

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A;Status: preliminary
A;Status: preliminary
A;Residues: 1-19 <cmt.
A;Residues: 1-19 <cmt.
A;Residues: 1-19 <cmt.
A;Cross-references: GB:MZ7814; NID:g200762; PIDN:AAA40060.1; PID:g200763
A;Cross-references: GB:MZ7814; NID:g200762; PIDN:AAA40060.1; PID:g200763
A;Cross-references: GB:MZ7814; NID:g200762; PIDN:AAA40060.1; PID:g200763
B;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific of A;Reference number: S22598; MUID:92107684; PMID:1840677
                                                                                                                                                                                                                chinchilla pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cjaces 30-Nov-1980 #sequence revision 13-Mar-1997 #text_change 18-Jun-1999 CjAcession: A34090; S22598; A00830 R;Schueller, C; Nijssen, H.M.J.; Kok, R.; Beintema, J.J. Mol. Biol. Evol. 7, 29-44, 1990 A;Fitle: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of A;Reference number: A34090; MUID:90136034; PMID:229980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQQKHI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
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A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
A; Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
A; Tibestra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A; Title: The amino acid sequence of mouse pancreatic ribonuclease.
A; Reference number: A00830; MUD:80024269; PMID:556267
A; Accession: A00830; MUD:80024269; PMID:556267
A; Accession: A00830
A; Molecule type: protein
A; Residues: 26-149 <LEN>
C; Superfamily: pancreatic ribonuclease
C; Seperfamily: pancreatic ribonuclease #status experimental <AMT>
F; 1-25/Domain: signal sequence #status predicted <SIG>F; 1-25/Domain: signal sequence #status predicted <SIG>F; 1-25/Domain: signal sequence #status predicted <F; 56-149/Arcdive site: His, Lys, His #status predicted F; 51-109, 65-120, 83-135, 90-97/Disidlide bonds: #status predicted F; 51-109, 65-120, 83-135, 90-97/Disidlide bonds: #status predicted F; 62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 L-----STTRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 103
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 FERGHMDSRGSPSTNPNYCNEMMKSR-NMTQSRCKPVNTFVHEPLADVQAVC---FQKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LCKNGQINCYQSNSNMHIIDCRVISNSDYPNCSYRISQEEKSIVVACEGNPYVPVHF
                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-128 < VAN>
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 26-64, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
F; 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
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19.4%; Score 116.5; DB 1; Length 149;
Best Local Similarity 29.9%; Pred. No. 0.00018;
Matches 35; Conservative 17; Mismatches 42; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 128;
                                                                                                                                                                                                                coypu and
                                                                                                                                 Rivan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Biochim. Biophys. Acta 453, 400-409, 1976
A/Title: Isolation, properties and primary structure of coyp A, Reference number: A90612; MUID:77065676; PMID:999896
A, Accession: A00822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 116.5; DB 1
Pred. No. 0.00015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5)
N'Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 1-128 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A34090
                                                                                                                 C; Accession: A00822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Bjechim. Blophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 1992
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A,Residues: 1-124 <BEI>
C;Superfamily: pancrearic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKRVNTFIISSATTVKAICTG----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98
               FORQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
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                                                                                                                                                                                                                                                                                                                                                                            C; Species: Sus scrofa domestica (domestic pig)
C; Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    66 NGRINC-YKSNSRLSITNCRQTGASKYPNCQXETSNLNKQIIVACEGQYVPVHF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database,
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                           52 TGVINLNVLSTTRFQLNTCTRISITPRP-CPYSSRIETNYICVKCENQY-PVHF
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39.5%; Pred. No. 9.3e-05;
tive 6; Mismatches 35;
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ilarity 29.9%; Pred. No. 9.3e-05;
Conservative 19; Mismatches 44
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Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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mouse

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엄 ð RESULT 13 NRCU

Query Match

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pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Decies: 19.mar-1997 #sequence_revision 19-mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W; Beintema, J.J.; Hofsteenge, J.
Bur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MJID:94139745; PMID:8307028
A;Accession: S41111
A;Actus: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                    58 NVL-----STTRFQLNTCTRISITPRP-CPXSSRTETNYICVKCE-NQY-PVHFA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ATFQORMI-----INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
                                                                                                                                                                                                                                                                                                                     87
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N.Alternate names: RNase 1; RNase A
N.Alternate names: RNase 1; RNase A
C.Species: Macropus rufus, Megaleia rufa (red kangaroo)
C.Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C.Accession: A00833
R.Gaastra, W.; Welling, G.W.; Beintema, J.J.
Blochem. 86, 209-217, 1998
A.Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A.Feference number: A00833; MUID:78190621; PMID:658039
                                                                                                                                                                                                                                                                        1 QNWATFQOKHI-----INTPIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAIC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS
                                                                                                                                                    Gaps
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A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease; nucleic acid digestion; pancrease; F:11,40,117/Active site: His, Lys, His #status predicted
F:25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                           23;
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                                                          Length 167;
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                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                        21.6%; Score 129.5; DB 2; 30.6%; Pred. No. 1e-05; ive 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
Query Match
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Thes 37; Conservative
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Matches 34; Conserv
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A; Molecule type: DNA
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A; Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
C; Watanabe, H.; Katoh, H.; Ishli, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iril
C; Watanabe, H.; Katoh, H.; Ishli, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iril
C; Watanabe, H.; Katoh, H.; Ishli, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iril
A; Reference number: JX0056; MUID:89214015; PMID:3243767
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A; Residues: 27-166, S', 166-
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A'Molecule type: protein
A'Residues: 1,'Q', 3-124 -JAC>
R'Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A'Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
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Nucleic Acids Res. 19, 6469-6474, 1991
A; Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex A; Reference number: S20066; MUID: 92093604; PMID: 1754384
                                                                                                                                                                                                                                                                                                                                   The amino acid
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C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The a A;Reference number: A92071; MUID:70104197; PMID:5460946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Contents: annotation, disulfide bonds
Cisuperfamily: pancreatic ribonuclease
Cisteywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F/12, 41,119/Active site: His, Lys, His #status predicted
F/21, 44,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
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C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
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Best Local Similarity 30.7%; Pred. No. 7.6e-06;
Matches 35; Conservative 20; Mismatches 42
                          - pig
             3.1.27.5) RNase A
    pancreatic ribonuclease
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pancreatic ribonuclease (EC 3.1.27.5) - minke whale pancreatic ribonuclease (EC 3.1.27.5) - minke whale placestate names: RNase 1; RNase A C; Species: Balaenoptera acutorostrata (minke whale, lesser rorqual) C; Species: Balaenoptera acutorostrata (minke whale, lesser rorqual) C; Species: Balaenoptera acutorostrata (minke whale, lesser rorqual) Balaets: 24-Apr-1994 #text_change 03-Jun-1994 C; Accession: A00818 R; Emmens, M.; Welling, G.W.; Beintema, J.J. Biochem, J. 157, 317-323, 1976 A; Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease. A; Reference number: A00818; MUID: 76277855; PMID: 962870 A; Reference number: A00818 A; Accession: A00818 A; Accession: A00818 A; Accession: A00818 A; Accession: A00818 A; Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accession: Accessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LCKNGRINCYESNSTWHIIDCRQIGSSKYPNCAYKISQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase, nucleic acid degradation; pyroglutamic
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAI>
F;25/Modified site: pyroolidone carboxylic acid (Gln) (in mature form) #stat
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQXHII------NTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NyAlternate names: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID: 91025023; PMID: 2222458
A;Accession: A35932.
                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: U22516; NID: 9726325; PIDN: AAA91366.1; PID: 9726326
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 21.9%; Score 131.5; DB 1
1 Similarity 32.5%; Pred. No. 4.8e-06;
38; Conservative 17; Mismatches 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.8%; Score 136.5; DB 1
40.3%; Pred. No. 1.8e-06;
iive 11; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                  A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 ETNYICVKCENOYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GFRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T.; Ohg
                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1,27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: 1400085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; O
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; O
A;Title, Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: 1X0085; MUID:90130374; PMID:2613682
A;Ancession: JX0085
A;Ancession: JX0085
A;Ancession: JX0085
A;Ancession: JX0085
C;Keywords: hypoclana, cacid
C;Keywords: hypoclana; pyrodlutamic acid
F;10,35,104/Active site: His, Lys, His #status predicted
F;10,35,104/Active site: His, Lys, His #status predicted
F;10,72,34-82,52-97,94-111/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribonnolease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Species: 31-011-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and A;Reference number: A39035; MUID:91093131; PMID:1985896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rana catesbeiana) liver.
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                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ONWAIFOOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.
                                                                                                                                                                                                       61 VLSTTRPQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 370; DB 2;
Pred. No. 1.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.7%; Score 370;
64.9%; Pred. No. 1
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-104 <ARD>
C,Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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Best Local Similarity
Tes 72; Conserve
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7;

5 RESULT

angiogenin precursor - mouse

'n RESULT A35932

Matches

g à

#status predicted

3

Gaps

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

7, 2004, 21:38:36 ; Search time 9.98129 Seconds

(without alignments)
1060.090 Million cell updates/sec

US-09-961-400-19 Perfect score:

600 1 QNWAIFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:* Database :

pir2:*
pir4:* pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

angiogenin - pig pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin [valida pancreatic ribonuc angiogenin precurs pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin - pig pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease-relat pancreatic ribonuc ribonuclease-relat angiogenin precurs pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic-type ri ribonuclease - dom pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc - rabbi Description angiogenin SUMMARIES A27121 JX0120 JX0085 A39035 A35932 NRWHK NRPG S20066 S41111 NRKGR A43825 NRPRH NRCU NRMS NRGPB A32474 NRCM NRCMM NRCMB NRCMB NRKS S08549 NRDEN B43825 NRDEO S22808 NRWB DB Query Match Length 128 128 128 128 128 130 130 4.1.0.0.0.0.0.0.0.4.0.0.1.1.0. 131.5 129.5 127.5 127.5 118.5 118.5 116.5 116.5 114.5 113.5 113.5 113.5 Score 451 112.5 110.5 109.5 109.5 108.5 108.5 108.5 Result No.

eosinophil-derived pancteatic Tibonuc		pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc seminal ribonuclea seminal ribonuclea	pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc
I61900 NRBOB NREKN	S07141 NRBO JX0115 NRSH	NRRT NRCB A47498 NRBOS	S04503 NRGN NRDEF S08546
2 4 4	2425	14444	2442
158 124 124	124 150 119	152 1224 125 126	125 124 124 124
17.9 17.8 17.8	17.8 17.8 17.6 17.6	17.6 17.4 17.2 17.2	16.8 16.8 16.8 16.8
107.5 106.5 106.5	106.5 106.5 105.5 105.5	105.5 104.5 103.5 103.5	100.5 100.5 100.5 100.5
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#### ALIGNMENTS

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ribonuclease-related sialic acid-binding lectin - bullfrog
C.Species: Rana catesbelana (bullfrog)
C.Species: Rana catesbelana (bullfrog)
C.Species: D.Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C.Accession: A27121
B.Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag Botchemistry 26, 2189-2194, 1987
A.Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbelana)
A.Reference number: A27121; MUID:87299649; PMID:3304421
A.Accession: A27121
A.Accession: LTTP
C.Superfamily: pancreatic ribonuclease
C.Superfamily: pancreatic ribonuclease

Gaps 1; Ouery Match
97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 1e-50;
Matches 107; Conservative 3; Mismatches 0; Indels 1;

7

ONWATFOOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59 ð

09 09 g à

LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110 

Tibonuclease-related sialic acid-binding lectin - Japanese frog C;Species: Rana japonica (Japanese frog) C;Species: Rana japonica (Japanese frog) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JX0120 F;Ramiya, Y.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990 A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs. A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A;Wolecule type: protein
A;Residues: 1-111 <KAM>
A;Esperimental Source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Gaps 5 Score 451; DB 1; Length 111; Pred. No. 1e-37; 8; Mismatches 15; Indels .. 75.2%; ilarity 77.5%; Conservative Query Match Best Local Similarity Matches 86; Conserv 96;

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1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                     1. EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKN 56
                                                                                                                                                                     9; Gaps
                                                                                                                                                                                                                                                                                                                                                        57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                             59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                  Query Match
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPINY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-28P-1993
FRIING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 03/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAMMP: Wahar Fillen Lawrer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 576-0200
INFORMATION FOR SEG ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 13, Application US/08891848; Patent No. 5955073; GENERAL INFORMATION:
, UKGANISM: Rana pipiens
;
UB-08-467-955-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-891-848-13
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1 QNWATEQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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                                                                                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07921619
Sequence 1, Application US/07921619
Patent No. 5555734
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: New YOLK
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURSILING DATE: 19207028
CLASSIFICATION NUMBER: US/07/921,619
FILING DATE: 19207028
CLASSIFICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1908
PRIOR APPLICATION NUMBER: US 07/178,118
FILING DATE: 13-NOV-1993
ATTORNEY AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION WUMBER: 2750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEPRORE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 718-625-0399
TELEX: No. 559574 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                              οκGANISM: Rana pipiens
;
US-08-283-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 104 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal
                                                                                                       N-terminal
                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: -
MOLECULE TYPE: pro
                  linear
                                                                                ANTI-SENSE: N
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-07-921-619-1
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1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                           59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                          Sequence 1, Application US/08467955
Sequence 1. Application US/08467955
GENERAL INFORMATION:
APPLICANT: Archael Ph.D, Wojciech J.
APPLICANT: Archael Ph.D, Wojciech J.
APPLICANT: ARCHAEL PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                           6
                                                                                  Length 104;
                                                                                                                         32; Indels
                                                                                  ch
1 Similarity 47.7%; Pred. No. 6.5e-24;
53; Conservative 17; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION NUMBER: US 07/436,141
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-MOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: No. 5728805 Applicable INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Mark H. Jay, P.A. STREET: P.O. BOX E CITY: Short Hills STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: 201-912-9066
              ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-912-0442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07078-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           US-08-467-955-1
                                           ;
US-07-921-619-1
                                                                                            Query Match
                                                                                                                                      Matches
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1 ONWATROCKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAIGTGVI-NLN 58
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APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
TUMBER OF SEQUENCES:
ADDRESSER: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                         Length 379;
                                                                                                                                                                                                                                                                                                                                                              ch 45.6%; Score 273.5; DB 3;
1 Similarity 48.6%; Pred. No. 1.4e-23;
54; Conservative 16; Mismatches 32;
                                     NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: JAY, MARK INFORMATION:
NAME: JAY, MARK INFORMATION:
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEX: No. 55.29775 Applicable INFORMATION FOR SEQ ID NO: 1: ERGUENCE CHARACTERISTICS: TYPE TYPE
                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          i LENGTH: 379 amino acids
i TYPE: amino acid
r TOPOLOGY: linear
i MOLECULE TYPE: protein
US-08-875-811-43
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 QDWLFPQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIXSRPEPVKALCKGIIASKN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rydak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Meddwer, Lluis
APPLICANT: Moddwer, Alexander
ITILE OF INVENTION: Recombinant Ribonuclease Proteins
ORRESPONDENCE ADDRESS: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: San Francisco
COURMEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834

COMPUTER EADABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US/08/11,800
FILING DATE: 21-FEB-1996
                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.6%; Score 273.5; DB 3 Best Local Similarity 48.6%; Pred. No. 3.8e-24; Matches 54; Conservative 16; Mismatches 32
                                                                                                                                                                                                                                                                                                           .
41,739
PP: 015280-244100US
                                                            APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01520
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-875-811-63
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-875-811-43
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USA
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US-08-875-811-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-095-429-1
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                          APPLICANT: Youle, Richard
APPLICANT: Youle, Richard
APPLICANT: Youle, Richard
APPLICANT: Washadau, Veena
APPLICANT: Wo. Yon-Neng
APPLICANT: Wo. Yon-Neng
APPLICANT: Boix, Ester
APPLICANT: Boix, Ester
APPLICANT: Boix, Ester
APPLICANT: Mois-sen
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
59 VLSTIRRQLNICIRISIIPRRPCPYSSRIEINYICVKCENQYPVHFAGIGRC 109
                              57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.6%; Score 273.5; DB 4; Length 1
48.6%; Pred. No. 2.9e-24;
tive 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IPM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RAN, DAVId B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09095429
Patent No. 6649393
GENERAL INFORMATION:
APPLICANT: Youle, Richard
                                                                                                                                               Sequence 1, Application US/08626288
Patent No. 6649392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vasandani, Veena
Wu, Yon-Neng
Boix, Ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 104 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 48.6
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-095-429-1
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                                                                                                                                      US-08-626-288-1
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1 QNWAJFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 VLTTSEPYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
APPLICANT: Ardelt, Wojelech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Frotein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
TUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Sequence 63, Application US/08875811

Selent No. 6045793

GENERAL INFORMATION:

APPLICANT: Rybar, Susanna M.

APPLICANT: Wewton, Liuis

APPLICANT: Wence, Liuis

APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       CMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
FILING DATE:
ATTORNEY/AGENT:
NAME: RAI, David B.
REGISTRATION NUMBER: 38,589
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 273.5; DB 4;
48.6%; Pred. No. 2.9e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street 1 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 104 amino acids
amino acid
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                                                                                                                                                                                                                                                         ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Sequence 1, Application US/09687748

Patent No. 6433515

GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K

TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFREENCE: 5013 US 01

CURRENT APPLICATION NUMBER: US/09/687,748

CURRENT PILING DATE: 2000-10-14

PRIOR APPLICATION NUMBER: 09/394,268

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver: 2.0
                                    QNWATEQORHINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/0968748

Patent No. 642315

GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K

TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01

CURRENT APPLICATION NUMBER: US/09/687,748

PRIOR FILING DATE: 2000-10-14

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0
                                                           1 ONWATEQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QNWATEQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                  59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at OTHER INFORMATION: position 72
                                                                                                             VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 104;
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1 Similarity 49.5%; Pred. No. 2.9e-24;
55; Conservative 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.6%; Score 273.5; DB 4 48.6%; Pred. No. 2.9e-24; cive 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 54; Conserv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 55, Conserve
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US-09-687-748-1
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US-09-687-748-1
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                                                                                                                                                   1 QNWATFQOKHINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIGTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: MUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VOY: 2.0
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09394268
Patent No. 6175003
Patent No. 6175003
Patent No. 6175003
Patent No. 6175003
Patent No. 6175003
Patent No. 6175003
Patent No. 6175003
PILLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF TITLE OF INVENTION: MAKING THEM CURRENT APPLICATION NUMBER: US/09/394,268
UURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOPTWARE: PatentIn Ver. 2.0
LENGTH: 104
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                                                                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                        59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                             DB 1; Length 104;
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Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9,
                                                                                                   31; Indels
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                                                   ch 46.8%; Score 280.5; DB 1 Similarity 48.6%; Pred. No. 4.5e-25; 54; Conservative 17; Mismatches 31
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Patent No. 6175003
   Oocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.6*
Matches 54; Conservative
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Rana pipiens
                                                                      Best Local Similarity
Matches 54; Conserv
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US-08-467-955-2
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                                                     Query Match
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4

Gaps

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26

Gaps

6

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ORGANISM: Rana pipiens
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-875-811-8
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US-08-467-955-2
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                                                                                                                                                                                                                                                                                                                    1 QUWATEQQKHILINTELI-CNTILDINILYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         60 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                61 LSTTRFQLMTCTRTSITPRPCPYSSRTEINVICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                               Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Nodawer, Lluis
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTED READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 12-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 12-FEB-1966
ATTONEY/AGENT INFORMATION:
                                                                                                                                            /note= "Frog Lectin from Rana
catesbeiana"
                                                                                                                                                                                                                               Query Match 97.1%; Score 582.5; DB 2; Best Local Similarity 96.4%; Pred. No. 6.4e-60; Matches 107; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Faris, Susan K. REGISTRATION NUMBER: 41,739
REGISTRANCE DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: 111 amino acids amino acids
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                                  TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein LOCATION: 1..111
                                                                                                                              LOCATION: 1..111
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                            Protein
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                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                            NAME/KEY:
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US-08-875-811-8
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1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08467955
Sequence 2, Application US/08467955
Barent No. 5728805
GENERAL INFORMATION:
APPLICANT Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE: ADDRESSE: STREET: P.O. Box E
CITY: Short Hills
STREET: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                              60 LSTTREQINTCTRISITERECPYSSRIETNYICVKCENQYEVHERGIGRCP 110
                                                                                                                                                                                                                                                                      61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                       1;
                                                                             Length 111;
                                                                                                                         0; Indels
/note= "Frog Lectin from Rana
catesbelana"
                                                                             97.1%; Score 582.5; DB 3; 96.4%; Pred. No. 6.4e-60; iive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR PAPLICATION 1435
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1989
PRIOR PAPLICATION DATE:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR PAPLICATION NATE:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASE #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: No. 5728805 Applicable INFORMATION FOR SEQ ID No: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201-912-0442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                          97.1
Best Local Similarity 96.4
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07078-0383
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - pr	OM protein - protein search, using sw model
Run on:	May 7, 2004, 21:28:45; Search time 12.7596 Seconds (Without alignments) 445.066 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-961-400-19 600 1 QNWAIFQCKHIINTPIICNTICVXCENOYPVHFAGIGRCP 110
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seg length: 0 Maximum DB seg length: 200000000

/cgm2_6/ptcdata/2/iaa/5A_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/PcTuS_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/PcTuS_COMB.pep:* Issued Patents AA: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Sequence 12, Appl	8	٠,	· -	٠,	equence 2,	ī	c,	Sequence 1, Appli	ı,	63	4	? -	ì,	Ť,	-ì	Ę	7	7	. 0	7	, ,	ď,	À,	7	Н	28	30	32	59
SUMMAKIES	ID		00.031-848-	-TT9-C/9-00-	-08-467-	US-09-394-268-1	-394-268-	09-687-748-	-04/ (80 %)-	000 000 000	70 007 400	00 001 020	9-TTR-6/9-8TT-6	-875-	US-08-283-971-1	US-07-921-619-1	08-46	α	1000	76-626-288-	79-095-429-	875-	US-08-875-811-41	US-08-875-811-51	112	19-071	011-380-00	-08-936-119-1	-08-87E 011	-TTB-070-00	-TTR-6/8-00-	US-08-875-811-59
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175-08-02E	T9-TT9-C/O 00 00	02-08-8/2-8II-48	TS-08-875-011 CT	/C-TTB-C/0 00 001	02-08-875-811-64	TS-08-875-011-65	T10 00 00 01	02-08-8/2-8TI-54	TIS-08-875-811-26	27 TTO C C C C C C C C C C C C C C C C C C	02-08-8/2-81T-45	US-08-875-811-53	110 000 001	02-08-8/2-811-20	TIS-08-875-011	77-110-010 00 00	US-09-223-118-3	TIS-08-875-811-47	710 000 000 011	02-03-773-TT8-2	IIS-09-223-118-1	1 0 1 1 CCC 00 1311	03-03-773-TT8-4	US-08-875-811-2	77 77 77 77 77 77 77 77 77 77 77 77 77	08-08-0/T-6/Z-3
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268.5	268.5		268.5	268 5		268.5	263.5		263.5	259.5		457.5	245 5	,	235.5	232	1 1	2.53.5	223	1 0	777	221	0	707	202	1
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#### ALIGNMENTS

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Sequence 12, Application US/08891848

Fatent No. 5955073

APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Notholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CIASSIPICATION NUMBER: US/08/891,848
FILING DATE: 22-SEP-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-CCT-1991
APPLICATION NUMBER: US 07/779,195
FILING DATE: 20-CT-1991
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DAR-1990
APPLICATION NUMBER: US 07/510,696
ATTORNEY/AGENT INPORMATION:
TELEPHONE: (415) 576-0200
INPORMATION FOR SED ID NO: 12:
EENGTH: 111 amino acids
TTELEFAX: (115) TRE-DATERISTICS:
LENGTH: 111 amino acids
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This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens occytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture selection agent, e.g. to identify gene therapy compositions able to
                                                                                                                                                                                                                                                                                                                                                                              Recombinant Onc protein with glutamine residue at position 1 - useful as antitumour and antiviral agent, also as cell culture selection agent.
                                                                                                                                                                                                                                                                                                                                                                                                            59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frog; ribonuclease; ranpirnase; RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31667 standard; protein; 104 AA
                                                                                                                                                                                                 Claim 1; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                     inhibit tumour growth
                                                                                                                                             WPI; 1997-512725/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                           Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6175003-B1
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2001
                                                            04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2001
                     WO9738112-A1
                                                                                 04-APR-1996;
 Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid
                                      16-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                          Youle RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB31667
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Conservative

Similarity

1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58

sequence of a modified frog ribonuclease protein.

(first entry)

/note= "wild type Met changed to Leu" 72 /note= "wild type Ser changed to Cys"

99US-00394268 99US-00394268

10-SEP-1999; 10-SEP-1999;

Location/Qualifiers

4;

9; Gaps

Indels

45.6%; Score 273.5; DB 2; 48.6%; Pred. No. 5.5e-23; ative 16; Mismatches 32;

Length 104;

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4;
                                                                                                   New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.
                                                                                                                                                                                        The present sequence represents a modified frog ribonuclease protein (ranpinnase) (RNase). The synthetic ribonuclease comprises a cysteine which facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification describes a method processing broduction of ranpinnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ONWAIFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 VLTTSEPYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VLSTTREQLATCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 109
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د
                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%; Score 273.5; DB 4; Length 104;
49.5%; Pred. No. 5.5e-23;
Live 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 7, 2004, 21:38:29 Job time: 47.9224 secs
                                                                                                                                                                  Claim 2; Col 5-6; 7pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Conservative
(ALFA-) ALFACELL CORP.
                                                                          WPI; 2001-167808/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104 AA;
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Ardelt W;

Boix E,

Wu Y,

Vasandani VM,

97WO-US005675. 96US-00626288

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI). Protein with Met at position 1. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hGG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana pipiens ribonuclease Clone 5alb; RaPLRI; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ONWATEQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 105;
                                                                                                                                                    note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%; Score 277.5; DB 2;
48.6%; Pred. No. 2e-23;
ive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens Clone Salb ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28879 standard; protein; 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 34; Page 57; 71pp; English.
                                                                                                                                                                                                                                             99WO-US006641
                                                                                                                                                                                                                                                                           98US-0079751P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Conservative
                                                                                                                                                                                                                                                                                                                                    Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-610847/52.
                                              autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ08126
                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105 AA;
                                                                              Rana pipiens.
                                                                                                                                                                                  WO9950398-A2
                                                                                                                                                                                                                                            26-MAR-1999;
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                                                                                                                                                                                                                07-OCT-1999
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                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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The present sequence is a Rana pipiens Clone Salb ribonuclease (RapLRI). It is encoded by Clone Salb CDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncomase (RTM) at amino acid covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic spanish choice against Choice against Kaposi's Sarcoma cells. Recombinant inconcleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to proteins to proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
ე
                                                                                                                 /label= Rana_pipiens_Clone_Salb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5e-23;
les 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%; Score 277.5; DB 2;
48.6%; Pred. No. 2.5e-23;
live 16; Mismatches 32;
                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                               1. .23
/label= Signal_peptide
/note= "Putative"
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 69; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW30301 standard; protein; 104 AA.
                                                                                                                                                                                                 99WO-US006641
                                                                                                                                                                                                                          98US-0079751P
                                                                                                        .127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant onc protein.
                                                                                                                                                                                                                                                                              Newton DL;
                                                                                                                                                                                                                                                                                                      WPI; 1999-610847/52.
autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ08136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 127 AA;
                          Rana pipiens.
                                                                                                                                            WO9950398-A2
                                                                                                                                                                                               26-MAR-1999;
                                                                                                                                                                                                                       27-MAR-1998;
                                                                                                                                                                     07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1998
                                                                                                                                                                                                                                                                             Rybak SM,
                                                              Peptide
                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW30301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW30301
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
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4

AAY28865

₫

(first entry)

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Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptied; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                   New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                       Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES
AAY28869 standard; protein; 105 AA
                                                                                                                 cancer; frog; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 59; 71pp; English
                                                                                                                                                                                                                                                                                                                                       Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                            1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ08127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 105 AA;
                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                             Misc-difference
                                                                                                                                     Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                                                                                                                                                                                           WO9950398-A2
                                      25-JAN-2000
                                                                                                                                                                                                                                                               07-OCT-1999
                    AAY28869;
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99WO-US006641. 98US-0079751P.

'note= "Met not found in wild type RaPLR1"

Location/Qualifiers

/note= "Wild type Met replaced with Leu"

```
The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein. Carboxy terminal end of RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (MCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moietles to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                            Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ODWLÍFOKKHLINIRDVDCNNÍMSINLF----HCKDKNIFIYSRPEPVKAICKGIÍASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QNWATFOOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VLSTIRFQLNICIRISIIPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.2%; Score 277.5; DB 2
48.6%; Pred. No. 1.9e-23;
:ive 16; Mismatches 32
                                                                                                           Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28867 standard; protein; 105 AA
Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 55; 71pp; English.
AAY28865 standard; protein; 104
                                                                                                                                                                                                                                                                                                                                                                                                             98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Met(-1) RaPLR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ08124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                                                                                                                         Rana pipiens
                                                                                                                                                                                                                                                                                              WO9950398-A2
                                                                           25-JAN-2000
                                                                                                                                                                                                                                                                                                                                  07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY28867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                        AAY28865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1:
AAY28867
    MXEXEXEXEX AXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a recombinant Rana pipiens ribonuclease protein (RapERI) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RapERI has a covalently bound ligand binding molety, which can be a LL2 antibody directed against CD22 or cancerous B cells or human chorionic gonadorrophin (hC3) effective expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moleties to form ovtotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                               note="(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNWATEQOKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLSTTREQLNTCTRTSITPRECPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9:
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4

58 26

> 1 RESULT

Length 105;

Indels

; Score 279.5; DB 2; ; Pred. No. 1.2e-23; 15; Mismatches 32;

46.6%;

Conservative

55;

Matches

g ₽ Recombinant RaPLR1 Met23Leu amino acid sequence.

(first entry)

25-JAN-2000

AAY28866 standard; protein; 104 AA.

RESULT 9

AAY28866

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1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the
                                                                                                       ONWAIFQOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
                                                                                                                     (Rana catesbeiana) lectin used to describe the method of the invention
                                                                                      Gaps
                                                                                                                                                        LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110
                                                                                                                                                                         ;
                                                            Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                   Indels
                                               Score 582.5; DB 2;
Pred. No. 6.5e-58;
Dred. No. 6.5e-58;
                                                                                                                                                                                                                                                                                                                           Antitumour protein from Rana pipiens oocytes.
                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                AAW06544 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Page 28; 45pp; English.
                                                       97.1%;
96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-00467955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US008304
                                                                Best Local Similarity 75.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043063/04.
                            Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                                                                                                                                   22~AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                       WO9639428-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996.
                                                                                                                                                         09
                                                                                                                                                                                                                                                                         AAW06544;
                                                     Query Match
                                                                                                                                                                                  61
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                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                     AAW06544
  2 X C
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Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu, covalently bound; LLZ antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kapoal's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met23Leu. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKKVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant ribonucleases, used for killing target cells, ating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                                                                                                                                                                                   /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e-23;
ches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 279.5;
Pred. No. 1.16
                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 34; Page 56; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                   99WO-US006641
                                                                                                                                                                                                                                                                                                                                           98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating cancers, viral
                                                                                                                                                                                                                                                                                                                                                                                                  Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-610847/52.
                                                                                                                                       autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 104 AA;
                                                                                                                                                                Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                             WO9950398-A2
                                                                                                                                                                                                                                                                                                                  26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                            27-MAR-1998;
                                                                                                                                                                                                                                                                                       07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
ò
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RESULT 10 AAY28869

1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58

EDWLTFQKKHVFNTRDVDCNNIMSTNLF----HCKDRNTFIYSRPEPVKALCKGIIASKN

VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109 

59

56

Gaps

6

Indels

Length 104;

DB 2; 31;

46.8%; Score 280.5; DB : 48.6%; Pred. No. 8.8e-24

17; Mismatches

Conservative

Local Similarity nes 54; Conserv

Best Loca Matches

₽ g  $\delta$ 

Query Match

. 0

Gaps

.;

Indels

0

2; Mismatches

Conservative

107;

g à g

0 61

Gaps

.. 0

0; Indels

Score 591; DB 2; Pred. No. 7.1e-59; 2; Mismatches 0;

Length 110;

Similarity

Query Match Best Local S Matches

Score 591; DB 2; Pred. No. 7.1e-59;

98.5%;

Length 111;

61

3 NWATFQQKHIINTPIICNTIMDNNIYIVGGGCKRVNTFIISSATTVKAICTGVINMNVLS 62

62 TTREQLATCTRISITERPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 110

2 NWATEQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS

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The present sequence is a recombinant Rana catesbeiana ribonuclease (RacORI) protein with Met at position 1 and Gln2Ser. Carboxy terminal of recombinant RacORI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1; covalently bound; Li2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
                                                                                                     2 NWATFQQKHIINTPIICNTIMDNNIXIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                   NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS
                                                                                                                                                     62 TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                      62 TTRFQLNTCTRISITPRECEYSSRTEINVICVKCENOYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Met not found in wild type RaCOR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                  Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                         AAY28878 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 68; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD22; RNase; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0079751P
                             98.5%;
98.2%;
                                                                                                                                                                                                                                                                                                                                          (first entry)
                           Query Match
Best Local Similarity 98.2
Matches 107; Conservative
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AA;
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Sequence 110
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                                                                                                                                                                                                                                                                                                           AAY28878;
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autoimmune diseases

Sequence 111 AA;

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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a vytotoxix agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                                                                                                                                                    Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain; heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; immune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinantly fused pancreatic RNase-targeting proteins useful for treating tumors, infections, immune or autoimmune disorders and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicholls PJ, Youle RJ;
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                                 AAY33321 standard; protein; 111
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91US-00779195.
93US-00014082.
                                                                                                                                        Frog lectin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                             97US-00891848
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                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-560488/47.
                                                                                                                                                                                                                                                                                                 Rana catesbeiana
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22-SEP-1993;
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                   AAY33321
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N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                         QNWATEQCKHIINTFILCNTIMDNNIYIVGGQCKRVNTFILSSATTVKALCTGVINMNVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease, RaCOR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thoundlease (RacOR1) protein with Met at position 1. Carboxy terminal and of recombinant RacOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells of thuman chorionic gonadorrophin (hCG) effective against Kaposi's sarcoma N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form
                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                        STIRFQLNICTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                              0;
                                                                                                                                                                                                                                                           present sequence is a recombinant Rana catesbelana oocyte
                                                                                                                                 Length 110;
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                                                                                                                                                           0; Indels
                                                                                                                         Score 596; DB 2;
Pred. No. 1.9e-59;
                                                                                                                                                      2; Mismatches
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                                                                                                                       99.3%;
98.2%;
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                                                                                                                                             Matches 108; Conservative
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                                                                                                                                  Local Similarity
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                                                                                      Sequence 110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; autoimmune disease.
  cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
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                                                                                                                                                  Gaps
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                                                                                                                                                                                   STIRPOLNICIRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 110
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                                                                              Length 111;
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0
                                                                       99.3%; Score 596; DB 2; 98.2%; Pred. No. 1.9e-59;
                                                                                                                                                                                                                                                                                                                                                                    Recombinant RaCOR1 Gln1Ser amino acid seguence.
                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                               AAY28877 standard; protein; 110 AA.
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                                                                                                 Conservative
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                                                                                   Similarity
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cytotoxic fusion
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                                         Sequence 111 AA;
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Best Local Simil
Matches 108; C
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Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic tusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL
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                                                                                                                                                                                                                                                                                            61 STTREQLNTCTRISITPRECPYSSRIETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                            Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
                                                                                                                                                                       , Score 600; DB 2; Length 110;
, Pred. No. 6.8e-60;
0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; bullfrog; RNase; autoimmune disease
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Matches 110; Conservative
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                                                                                                                     autoimmune diseases
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                                                                                                                                                 Sequence 110 AA;
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The present sequence is a Rana catesbelana oocyte ribonuclease (RacOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RacOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an
The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, Met23Leu and Met5BLeu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moietry, which can be a LL2 antibody directed against CD2 on cancerous B cells or human chorionic gonadotrophin (hcG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
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                                                                                                                                                                                                                                                                                                                                                           1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 STTRFQLNTCTRTSIIPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
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100.0%; Pred. No. 6.8e-60;
ive 0; Mismatches 0;
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Matches 110; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

model OM protein - protein search, using sw

May Run on:

7, 2004, 21:25:55 ; Search time 46.9224 Seconds (without alignments) 662.376 Million cell updates/sec

US-09-961-400-19 Title: Perfect

score:

1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP Sequence:

110

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Total number of hits satisfying chosen parameters;

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq 29Jan04:* geneseqp1980s;*
geneseqp1990s;*
geneseqp2000s;* geneseqp20028:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as;*geneseqp2003bs;*

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## ALIGNMENTS

Recombinant Rana catesbeiana oocyte ribonuclease, covalently bound, RaCORI Met22Leu Met57Leu, LL2 antibody, ligand binding moiety, CD22, cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease. Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence. /note= "Wild type Met replaced with Leu" Misc-difference 57/note= "Wild type Met replaced with Leu" AAY28874 standard; protein; 110 AA. Location/Qualifiers 99WO-US006641. (first entry) Rana catesbeiana. Misc-difference 25-JAN-2000 26-MAR-1999; W09950398-A2 07-OCT-1999. Synthetic. AAY28874; 

(USSH ) US DEPT HEALTH & HUMAN SERVICES. 98US-0079751P. Rybak SM, Newton DL; WPI; 1999-610847/52. N-PSDB; AAZ08132. 27-MAR-1998;

for e.g. New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 64; 71pp; English.

The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety,

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RR Beintema J.J.;

RI "Secretory ribonucless genes and pseudogenes in true ruminants.";

RI Gene 212:359-268(1998).

CC --- SUNCELLULAR LOCATION: Secreted.

--- SUNCELLULARIZE LOCATION: Secreted.

CC --- SIMILARIY: Belongs to the pancretic ribonuclease family.

CC --- SIMILARIY: Belongs to the pancretic ribonuclease family.

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BREST: Y11670; CAA72368.1; -- CC cor send an email to license@isb-sib.ch).

BREST: NOTOGY; RNASEA; 1.- CC cor send an email to license@isb-sib.ch).

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BREST: SMO0075; RNASEA; 1.- CC cor send correction.

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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
Giraffidae; Giraffa.
NCBI_TaxID=9894;
                                                                                                                                    MEDLINES/1970, FUND M.D., Vallee B.L.;

Strydom D.J. Bond M.D., Vallee B.L.;

"An angiogenic protein from bovine serum and milk -- purification and primary structure of angiogenin-2.";

Eur. J. Biochem. 247:535-544(1997).

Eur. J. Biochem. 247:535-544(1997).

-! FUNCTION: Binds tightly to placental ribonuclease inhibitor and as very low ribonuclease activity. Has potent angiogenic activity. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-! TISSUE SPECIFICITY: Serum and milk.
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MEDLINE=96139017; PubMed=8587129;
MCDLINE=96139017; PubMed=8587129;
MCDrfalnon E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M., Vonfalon M.T., Furia A.,
"Molecular evolution of genes encoding ribonucleases in ruminant
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
NCBI_TaxID=9913;
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14522 MW; B703B9839919FDZF CRC64;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                  Interpro, IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODOM; PD000535; RNaseA; 1.
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SEQUENCE OF 31-114 FROM N.A.

MEDLINE-93367815; PubMed=8360916;
Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
Carsana A., Palmieri M., Furia A.;
"Sequences related to the ox pancreatic ribonuclease coding region in
the genomic DNA of mammalian species.";
J. Mol. Evol. 37:29-35(1993).
-: SUBCELLUIAR LOCATION: Secreted.
-: SIMILARITY: Belongs to the pancreatic ribonuclease family.
-: SIMILARITY: Belongs to the pancreatic ribonuclease family.
-: SIMILARITY: Belongs to the pancreatic ribonuclease family.
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O-LINKED (BY SIMILARITY).
73745EFE9079591F CRC64;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.0%; Score 127.5; DB 1.
30.6%; Pred. No. 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 84
40 95
40 95
72 110
62 1
15592 MW; 7
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S81743; AAB36137.1; -. EMBL; S65126; AAB27931.1; -. HSSP; P00656; ZRNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.6
nes 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Axis porcinus (Hog deer)
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Beintema J.J.
                    RNBR_CAPCA
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                                                      FOOKHI-----INTPLICUTIMDNNIYIVGGOCKRVNIFIISSATTVKAICTGV-INMN 59
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                                                                  2 ONWATEQOKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ODWSSFONKHIDYPETSASNPNAYCDLMMORR-NLNPTKCKTRNTFVHASPSEIQQVCGS
                                                                                          60 VLSTTRFQLNT-----CTRTSITPRP-CPXSSRTETNYICVKCENQ--YPVHF 104
                                                                                                       67 NGQINCYQSNSTWHIIDCRQIGSSKYENCAYKASQBQKHIIVACEGNPPVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 --IGVINMNVLSTTRFQLNTCTRTSIT-PRPCPXSSRTETNYICVKCENQYPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GGTHYEDNLYDSNESFDLTDCYRNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                     3'-
U-P
                                                                                                                                                                                                                Iguana iguana (Common iguana).

Lebidosauria, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana.
                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 219:641-646(1994).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2', 3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TASUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
BIR; 541111; 541111.
                       DB 1; Length 124;
                                                                                                                                                                                                                                                                                        Zhao W., Beintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 119;
                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                        42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
  OAC28CDE14111845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6072FB5B7B15BD5A CRC64;
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                  21.8%; Score 132.5; DB 31.6%; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131.5; DB 1; Pred. No. 2.5e-07; 16; Mismatches 51
                                      19; Mismatches
                                                                                                                                                               119 AA
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MEDLINE=94139745; PubMed=8307028;
 13804 MW;
                                                                                                                                                                            (Rel. 28, Created)
(Rel. 28, Last seq
(Rel. 41, Last ann
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30.4%;
                                     36; Conservative
                                                                                                                                                           STANDARD;
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               Query Match
Best Local Similarity
124 AA;
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Eur. J. Bioch
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SEQUENCE
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P80287
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 NVL-----STIRFQLNICIRISITPRP-CPYSSRIEINYICVKCENQ--YPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NITCKNGQPNCYQSNSTWNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AKFRROHMDSGSSSSGNPNYCNOMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK
           P79351;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
Capreolus capreolus (Roe deer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                          "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212:255-268(1998).
-!- SUBCELIGIAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98278842; PubMed=9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .) (BY
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    151 AA.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 128.5;
Pred. No. 6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y11673; CAA72371.1; -. HSSP; P00656; 1SRN.
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29.4%;
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STANDARD:
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DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig)
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38;
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                                                                                                                                  106
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RNP_PIG
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                                                                                                                                  MEDLINE=92093604; PubMed=1754384; Sasso M.P., Carsara A., Confalone E., Cosi C., Sorrentino S., Viola M.P., Palmieri M., Russo E., Furia A.; "Molecular cloning of the gene encoding the bovine brain ribonuclease and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474(1991).
                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                          Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 27-167 FROM N.A.
MEDLINE=96139017; PubMed=8587129;
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                         Vento M.T., Furia A.; "Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 133.5; DB 1; Length 167; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                             _r_wol. Evol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                   "Primary structure of a ribonuclease from bovine brain.";
J. Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
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681CAAC3CC2FC459 CRC64;
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BY SIMILARITY.
A'LINKED (GLONAC. ..).
/FTIG=CAR_000005.
                                                                                                                                                                                                                                    SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBONUCLEASE, BRAIN.
BY SIMILARITY.
BY SIMILARITY.
        16-0CT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (BC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-LINKED
                                                                                                                                                                                                                                                                    MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P00656; ZRNS.
GlycoSuiteDB; P39873; -.
InterPro; IPR01427; RNaseA.
PFam; PF00074; KNaseA: 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA: 1.
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EMBL; S81744; AAB36138.1; -.
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167
38
67
145
110
121
136
98
                                                                             Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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159
155
167 AA;
                                                  Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                             Ohgi K., Irie M.;
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27
38
67
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                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                         rissum=Brain;
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22.0%; 31.4%;

Best Local Similarity

Query Match

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7 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISION TO 2. Wherenga R.E., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J., Wherenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J., "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence.";
                          5 ATFOOKHI-----INTPLICNTIMDNNIYIVGGOCKRUNTFILSSATTUKALCTGVINM
                                            32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKFVNTFVHESLDDVKAVCS---QK
                                                                                    ---SITRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHFA
 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                   Bukaryota: Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 245:654-661(1970).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphate intermediates.

-!- SUBCELDULAR LOCATION: Secreted.
-!- SUBCELDULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=70104198; PubMed=4904878;
Phelan J.C., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. 3.
disulfide_bonds.";
                                                                                                                                                                                                                                                                                21-101-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
 43; Indels
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DISULFID 26 84
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BY SIMILARITY.
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N-LINKED (GLCNA
N-LINKED (GLCNA
N-LINKED (GLCNA
    Conservative 17; Mismatches
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PROSITE, PS00127, RNASE PANCREATIC, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=70104197; PubMed=5460946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A22071; NRPG.
HSSP; P00656; 1SRN.
InterPro; IPRO01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                         STANDARD;
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RNBR BOVIN
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RY SEQUENCE FROM N.A.

RY STRAIN=FVB/N; TISSUE=Liver;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Wabin G.M., Hoop L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoop L.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Raha S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Raha S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Halach S.W., Woung A.C., Shevchenko Y., Bolifard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Siller Handth
                                                                                                                                                                                                                                                                                  7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMAV 60
                                                                                                                                                                                                                                                                                                    ---STTRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                 64 LCKNGRTNCYESNSTMHITDGROTGSSKYPNGAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                   23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                   22.3%; Score 135.5; DB 1; Length 124; llarity 33.3%; Pred. No. 9.5e-08; Conservative 16; Mismatches 39; Indels 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                           84 BY SIMILARITY.
95 BY SIMILARITY.
110 BY SIMILARITY.
72 BY SIMILARITY.
41 BY SIMILARITY.
119 BY SIMILARITY.
119 BY SIMILARITY.
119 BY SIMILARITY.
76 N-LINKED (GLCNAC. . .) (30%)
7, 14125 NW, F57475459F697E20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91025023; PubMed=22222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                    Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                             145 AA
                                PEAM; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCKEATIC;
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           HSSP; P00656; ISRN.
InterPro; IPR001427; RNaseA.
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                                                                                               Hydrolase; Nuclease;
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  PIR; A00818; NRWHK.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation use by non-profit institutions as long as its content is in no madified and this statement is not removed. Usage by and for commercial or sentities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSFFQVTTCKHTGGSPRPFCQYRASAG 122
                                                                                                                                                                                                  regions.",
Biochim. Blophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-!- SUBCELLULAR LOCATION: Secreted.
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Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                        TISSUB=Serum;
MEDLINE=591929291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
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PYRROLIDONE CARBOXYLIC ACID (BY
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cive 12; Mismatches 29; Indels
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human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(Rel. 31, Last sequence update)
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EMBL; BC055355; AAH55355.1; -.
EIR, A35932, A35932.
HSSP; P03950; 1A4Y.
MGD; MGI:88022; Ang.
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137 BY
104 BY
115 BY
130 BY
1628 MW;
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                                                                   PARTIAL SEQUENCE.
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P39873;
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P00673;
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                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=129; TISSUB=Liver;
MEDLINE=96079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
Brown G., Subramanian V., Structures of an angiogenin-related protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKRVNTFIISSATTVKAIC-----TGVINMNVLSTTRFQLNTCTRISITPR-PCPYSSR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                         Mol. Cell. Biol. 17:1503-1512(1997).

-!- FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endonuclease; Angiogenesis;
hibitor; Signal; Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANGIOGENIN-3.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
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          developmentally regulated genes when expressed in NIH 3T3
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Pred. No. 1e-09;
2; Mismatches 23;
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01-NOV-1997 (Rel. 35, Last sequ
28-FEB-2003 (Rel. 41, Last anno
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43.6%;
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SIGNAL 1 24
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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HSSP; P10152; 1AGI.
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SMART; SM00092; RNASE PC;
PROSITE; PS00127; RNASE_PA
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Biochem. J. 157:317-323(1976).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphoel intermediates.

-!- SUBCELIULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Pancreas.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
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N
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGIOGENIN-RELATED PROTEIN. PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A) RNASE1 OR RNS1.
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An 4%; Pred. No. 3.5e-09;
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21-1011-1986 (Rel. 01, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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BY SIMILARITY.
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BY SIMILARITY.
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Pyrrolidone carboxylic acid. POTENTIAL.
25 145 NUCLEALN
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PRINTS; PR00794; RIBONUCLEASE.
PRODON: PD000055; RNASEA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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InterPro; IPR001427; RNaseA.
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HSSP; P03950; 1A4Y.
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                                                                                                                                                                                                                                                                                                                 Gaps
        -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; JX0085; JX0085.
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a novel antitumor protein of Rana pipiens oocytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94166079; PubMed=8120892; Mosimann S.C., Ardelt W., James M.N.G.; "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity."; J. Mol. Biol. 236:1141-1153 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                            60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRG 110
                                                                                                                                                                                                                                                                                                                                                          61 ELSTISFKLNICIRDSITPRPCFYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                      Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
ACT_SITE 10 BY SIMILARITY.
                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93066156; PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                                                 Length 111;
                                                                                                                                                                                                                                                                                   27; Indels
                                                                                                                                                                                                                                        D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                            Score 374; DB 1;
Pred. No. 1.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 19, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
P-30 protein (EC 3.1.27.-) (Onconase).
Rana pipiens (Northern leopard frog).
                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
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PY SIMILARITY.
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                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91093131; PubMed=1985896;
 J. Biochem. 106:729-735(1989).
                                                                                                                                                                                                                                       12461 MW;
                                                                                 InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
                                                                                                                                                                                                                                                                     65.88;
                                                                                                                                                                                                                                                              61.68;
                                                                                                                  SMART; SM00092; RNASE PC;
PROSITE; PS00127; RNASE PP
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           embryos.";
Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                         HSSP; P11916; 1BC4.
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                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                  104
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                                                                                                                                                                                                                                        111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           James M.N.G.;
                                                                                                                                                                                                                                                                              73;
                                                                                                                                                                                                                                                                                                                                                                                                                     RN30 RANPI
                                                                                                                                                                                          DISULFID
                                                                                                                                                                      SITE
                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                      SEQUENCE
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Matches
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-!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vitro. It exhibits a ribonuclease-like activity against high "vitro lide with stranger a ribonuclease-like activity against high "C -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage). C -!- SIMILARITY: Belongs to the pancreatic ribonuclease family. RDB: 10NC; 31-JAN-94.

InterPro; IPR001427; RNASEA.

R Probom; PD000535; RNASEA.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R PYTCOLIGONE carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
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1 QDWLFPQKKHITNTRDVDCDNIMSTNLF.---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNWATEQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Last annotation update)
Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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"E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.2e-23;
Fred. No. 4.2e-23;
Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
MEDLINE=97184476; PubMed=9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                        68
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70
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01-NOV-1997
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                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASE PC; 1.
SPROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 133;
                                                                                                         -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 591.5; DB 1;
Pred. No. 9.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                        RIBONUCLEASE, OOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Signal; Pyrrolidone carboxylic acid. SIGNAL
                                                                                      SUBUNIT: Monomer. Subcellular LOCATION: Secreted.
                                                                                                                                                                                                                                              EMBL; AF039104; AAD10702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.4%;
99.1%;
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ProDom; PD000535; RNaseA; 1.
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PDB; 1BC4; 28-OCT-98.
PDB; 1M07; 21-JAN-03.
InterPro; IPR001427; RNaseA.
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SEQUENCE
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Created)
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(Rel. 16, (Rel. 28, 1) (Rel. 42, 1)

01-FEB-1994 10-OCT-2003

RANJA

RESULT 2

LECS RAN P18839;

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DT 01-NOV

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MEDLINE=90130374; PubMed=2613682;
Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
Okazaki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbelana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QNWAJFQQKHINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K., "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana
            Rana japonica (Japanese reddish frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 VLSTTRFQLNTCTRTSITPRPCPYSSRTBINYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 455; DB 1; Length 11 Pred. No. 3.7e-42; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWART; SM00092; RNASe Ps; 1.
PROSITE; PS00127; RNASE Psi 2.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; Pyrrolidone carboxylic acid.
MOD RES
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Sialic acid-binding lectin (EC 3.1.27.-).
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Rana catesbeiana (Bull frog).
                                                                                                                                                                     TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY
                                                                                                                                         SEQUENCE, AND DISULFIDE BONDS.
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                                                                                                  NCBI_TaxID=8402
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May Run on:

7, 2004, 21:30:40 ; Search time 5.60711 Seconds (without alignments) 1030.796 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-961-400-17
607
1 MONWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				catesb	Japoni	catesb	Pipien	musculu	musculu	balaenopter	musculu	taurus	scrofa	jgna	lus c	urus	a cam	porcin	i sci	hecus	ries	capra	ithec	ns rn	tor c	sculu	trivi	pygma	scrofa	porce	as oe	cabal	s dro	imys	ırus	mula
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		Description		PLISTE	P18839	F14626	P22069	P97802	Q64438	P00673	P21570	P39873	P00671	782084	P/9351	P80929	029542	P87350	Q8wn60	Q8wn65	029543	P00668	08wn66	P00686	P00676	P00683	C8WD61	08wn67	P31346	P00679	08wn62	P00674	F00670	on t	٠,	Cawiib3
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		Score	591.5	455	374	277.5	154.5	149.5	135.5	135.5	133.5	132.5	131.5	128.5	127.5	127.5	127.5	125	124	123.5	122.5	122.5	122	120.5	ς.	120	120	φ.	118.5	118	117.5	9	16.	115.5	Š.	
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P10152 P00566 Q8wn64 P03950 Q8wme8 P00664 P00664 P00664 P1117 P21347 P2117 P21717 P21717 P21717
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## ALIGNMENTS

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34 CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
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89 TNYICVKCENQYPVHF 104

à

99 FRTIAVACENGLPVHF 114

parcreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)

NAAlternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
C;Accession: A00826
Bur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a A;Reference number: A91247; MuID:77185023; PMID:862624

A, Molecule type: protein
A, Residues: 1-128 < VAN.
A, Residues: 1-128 < VAN.
A, Note: 64-Para at also found
C, Superfamily: pancreatic ribonuclease
C, Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas
F, 12, 4, 119/Active site: His, Lys, His #status predicted
F, 21, 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F, 26-84, 40-95, 58-110, 65-72/ pisulfide bonds: #status predicted

Gaps Query Match
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23;

9

7 FOOKHI-----INTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV 60 

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7, 2004, 21:54:55 Search completed: May Job time: 10.072 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHF 104
                                               Dancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N'Alternate names: RNase 1; RNase A
C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Accession: A34090; 822598; A00830
R'Schweller, C; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Nol. Biol. Evol. 7, 29-44, 1990
A,Title: Evolution of nucleic acids coding for ribonucleases: the mRNA seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982 A;Cross-references: EMBL: J.J. Beintema, J.J. Beintema, J.J. Biochem. 98, 399-408, 1979 A;Title: The amino acid sequence of mouse pancreatic ribonuclease. A;Reference number: A00830; MUID:80024269; PMID:S56267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database,
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 26-149 <LEN>
C,Superfamily: pancreatic ribonuclease
C,Superfamily: pancreatic ribonuclease nucleic acid digestion; pancrease
F;1-25/Domain: signal sequence #status predicted <2160>
F;2-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37 64,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
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A; Residues: 1-149 <SCH>
A; Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1;
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Pred. No. 6.5e-05;
6; Mismatches 35;
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Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42.
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39.5%;
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Best Local Similarity 39.5
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-149 <SAM>
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A,Status: preliminary
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NyAlternate names: RNase 1; RNase A
C; Species: Myocastor coppus (nutria, coypu)
C; Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C; Accession: A00822
R; van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys: Acta 453, 400-409; 1976
A; Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A; Reference number: A90822
A; McCession: A00822
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                                                                                                                                                                          NVACKNGQINCYQSYSIMSIIDCRETGSSKYPNCAYKITQAKKHIIVACEGNPYVPVHY 120
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AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61
                                                                                              --STIRFOLNICIRISITPRP-CPYSSRIEINYICVKCE-NOY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---STIRFQLNTCIRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQXHI-----INTPILCHTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                                                                                                                                                                                                                                                                                                                          pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1, RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 FOR CHADTEHSTASSSNYCHLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A00833
A;Accession: A00833
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGRINC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF
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R, Gaastra, W.; Welling, G.W.; Beintema, J.J.
Bur, J. Biochem. 86, 209-217, 1978
A, Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A, Reference number: A00833; MUID: 78190621; PMID: 658039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FOOKHI-----INTPLICUTIMDNNIYIVGGOCKRVNTFILSSATTVKALC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.9%; Score 120.5; DB 1; 31.6%; Pred. No. 5.4e-05; ive 15; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
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Indels 17;

Length 124;

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C,Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C'Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998 C'Accession: 841111 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998 By:Zhao, W.; Beintema, J.J.; Hofsteenge, J. Bur. J. Blochem. 219, 641-646, 1994 A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease. A;Reference number: 841111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/pisulfide bonds: #status predicted F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
   C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                          7 FOORHI-----INTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INMN
                                                                                                                                                                                                                                                                                                                   N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ONWATFOOKHI-----INTPLICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAIC--
                                                                                                                                                                                                                                                                                                                                                                                                                                        67 NGQTNCYQSNSTWHITDCRQIGSSKYPNCAYKASQBQKHIIVACEGNPPVPHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 --TGVINMAVLSTIRFQLNTCIRISIT-PRPCPYSSRIEINYICVKCENQYPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                  60 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTEINYICVKCENQ--YPVHF 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic ribonuclease (BC 3.1.27.5) - pronghorn (tentative sequence)
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                                                                                                                                                                                                                              42;
                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                 Pred. No. 3.3e-06;
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30.3%; Pred. No. 3.3e-05;
iive 18; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.7%; Score 131.5; DB 30.4%; Pred. No. 4e-06; ive 16; Mismatches !
                                                                                                                                                           th 21.8%; Score 132.5; D
| Similarity 31.6%; Pred. No. 3.3e-
36; Conservative 19; Mismatches
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A,Molecule type: protein
A,Residues: 1-119 <ZHA>
C,Superfamily: pancreatic ribonuclease
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                                                                                                                                                     Query Match
Best Local Similarity
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1.167 < cSAS
A; Cross-references: EMBL: X59767; NID: 9150; PIDN: CAA42439.1; PID: 9151
A; Matanabe, H.; Katch, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Irii
J. Biochem. 104, 939-945, 1988
A; Title: Primary structure of a ribonuclease from bovine brain.
A; Accession: JX0056
A; Molecule type: protein
A; Molecule type: protein
A; Rosidues: 27-154, S', 155-166 < WAT>
A; Rosidues: 27-154, S', 155-166 < WAT>
A; Rosidues: 27-154, S', 155-166 < WAT>
A; Rosidues: 27-154, S', 155-166 < WAT>
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A; Rosidues: 27-154, S', 155-166 < WAT>
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A; Rosidues: 27-154, S', 155-166 < WAT>
A; Rosidues: 27-
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                                                                                                                                  C.; Sorrentino, S.; Viola, M.; Palmieri
                      Cispecies: Bos primigenius taurus (cattle)
Cibate: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
Cibate: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
CiAccession: S20066; JX0056
RiSasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmie Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its A;Reference number: S20066; MUID:92093604; PMID:1754384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVL-----STTRFQLNTCTRISITPRP-CPYSSRTEINYICYKCE-NQY-PVHFA 105
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| AKPRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK
               BRb precursor, brain - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **Jaboriaminar Bource: District Thouselease C;Superfamily: pancrain ribonuclease C;Superfamily: pancrain ribonuclease C;Keywords: glycoprotein; hydrolase F;38-67,145/Active site: His, Lys, His #status predicted F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Pred, No. 3.6e-06;
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         (EC 3.1.27.5)
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N.Alternate names: RNase 1; RNase A
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31.4%;
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Best Local Similarity 31.48
Matches 38; Conservative
pancreatic-type ribonuclease
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N;Alternate names: angiogenesis factor
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R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
A;Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens occytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
                                                                                                                                                                                                                                                                                                                                                         pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
Cispecies: Rana catesbeiana (bullfrog)
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Cispecies: Rana catesbeiana (bullfrog)
Cispecies: Rana catesbeiana (bullfrog)
Cispecies: No. Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
Cispecies: Use of the company of the catesbeiana (cispecies)
Cispecies: Rana catesbeiana (cispecies)
Cispecies: Timary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
Cispecies: Drotein
Cispecies: L-111 < NUTC: Cispecies: Land of the catesbeiana (cispecies)
Cispecies: L-111 < NUTC: Cispecies: Land of the catesbeiana (cispecies)
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QNWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
                                      2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NNN
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C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 111,
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48.6%; Pred. No. 2.1e-20;
iive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.6%; Score 374; DB 2;
65.8%; Pred. No. 2.8e-30;
tive 9; Mismatches 27
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A;MoLecule type: protein
Kesidues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 FOROHMDSGNSPGNNPNYCNOMMRR-KMTGGRCKPVNTFVHESLEDVKAVCS---QKNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 L-----STTREQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LCKNGRINCYESNSTWHIIDCRQIGSSKYPNCAYKISQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITPR-PCPYSSRTE
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
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                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: protein
A, Readidues: 1-124 cEMM>
C, Superfamily: parcreatic ribonuclease
C, Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancre
F;12-14,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
                                                                                                                                                                                                                                                                 rorqual)
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30.5%; Pred. No. 2e-06;
                                                                                                     C,Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Fitte: The amino acid sequence of pike whale (lesser A;Reference number: A00818; MUID:76277855; PMID:962870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 135.5; DB 1
Pred. No. 1.7e-06;
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A; Status: not compared with conceptual translation A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Scor.
33.3%; Pred. No. 1...
16; Mismatches
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5

RESULT

pancreatic ribonuclease (EC 3.1.27.5) - minke whale

RESULT 5.

5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2004 Copyright

OM protein - protein search, using sw model

Run on:

(without alignments)
1060.090 Million cell updates/sec 7, 2004, 21:38:36; Search time 10.072 Seconds

US-09-961-400-17 Title: Perfect score:

1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pancreatic-type ri pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease-relat ribonuclease-relat pancreatic ribonuc ribonuclease-relat pancreatic ribonuc angiogenin precurs pancreatic ribonuc pancreatic ribonuc angiogenin. - pig pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease - dom pancreatic ribonuc angiogenin [valida pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin - rabbi pancreatic ribonuc pancreatic ribonuc angiogenin precurs Description SUMMARIES JX0120 JX0085 A39035 NRWHK S41111 NRPRH NRKGR NRCU NRMS A43825 A35932 S20066 NRPG NRHO
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ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87298649; PMID:3304421

A; Molecule type: protein A; Residues: 1-111 <TIT>

A) Residues: 1-111 (TIT) C) Superfamily: pancreatic ribonuclease C; Keywords: lectin

Gaps 1; Score 588.5; DB 2; Length 111; Pred. No. 1.3e-51; 1; Mismatches 0; Indels 1 97.0%; 98.2%; Best Local Similarity 98.2 Matches 109; Conservative Query Match

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2 QNWAIFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60 d à

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CiSpecies: Rana japonica (Vapanese frog)
CiSpecies: Rana japonica (Vapanese frog)
CiSpecies: Rana japonica (Vapanese frog)
CiSpecies: Rana japonica (Vapanese frog)
CiSpecies: Rana japonica (Vapanese frog)
CiSpecies: Rana japonica (Vapanese frog)
CiAccession: USC0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Accession: USC120
A;Accession: USC120
A;Molecule type: protein
A;Residues: 1-111 < KAM>
A;Residues: 1-111 < KAM>
A;Residues: 1-111 < KAM>
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pancreatic ribonuclease
C;Superfamily: pyrogiutamic acid
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Gaps 75.0%; Score 455; DB 1; Length 111; conservative 7; Mismatches 15; Indels 1 Similarity 87; Conserv Query Match Best Local S: Matches 87;

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TYPE: PRT

CREANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
COTHER INFORMATION: Met(-1) RapLR1)

US-09-948-391A-6
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4; Query Match
47.2%; Score 286.5; DB 10; Length 105;
Best Local Similarity 50.0%; Pred. No. 7.5e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps

QQ ð

Search completed: May 7, 2004, 21:51:58 Job time: 36.6155 secs

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61 STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                             US-09-948-391A-19
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                                 APPLICANT: GOLDENBERG, ANTID.

APPLICANT: GOLDENBERG, ANTID.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

CURRENT APPLICATION WUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION WUMBER: 09/622,613

PRIOR APPLICATION WUMBER: 09/622,613

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE PREAINT VET. 2010
SOFTWARE: PARCHIN VET. 2.1
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Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.1e-60; Mismatches 0;
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98.2%; Pred. No. 4e-60;
tive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 597; DB 10;
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%;
                       SUSANNA M.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 109, Conservative
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.2;
Matches 108; Conservative
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ORGANISM: Rana catesbeiana
GENERAL INFORMATION:
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US-09-961-400-24
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US-09-961-400-19
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52 STTRFQLNTCTRISITPRPCPYSSRTEINXICVKCENOYPVHFAGIGRCP 111

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QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNUL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbelana ribonuclease with Met22Leu and ... OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1 US-09-948-391A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.2%; Score 590; DB 10; Length 110; 97.3%; Pred. No. 2e-59; ive 2; Mismatches 1; Indels
                                                                                                        APPLICANT: Newton, Disamus I.,
APPLICANT: Newton, Disamus I.,
APPLICANT: Newton, Disamus I.,
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
TITLE OF INVENTION: Recombinant Auti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 00/079,751
PRIOR APPLICATION NUMBER: US 00/079,751
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 19
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APPLICANT: Newton, Dianne I.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
IITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERRING: 015260-34110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT PILING DATE: 2002-05-10
PRIOR FILING DATE: 1999-03-26
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PRIOR FILING DATE: 1090-03-26
PRIOR FILING DATE: 1090-03-26
PRIOR FILING DATE: 1090-03-26
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PRIOR FILING DATE: 1090-03-26
PRIOR FILING DATE: 1090-03-26
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PRIOR FILING DATE: 1090-03-26
PRIOR FILING DATE: 2000-08-17
Sequence 19, Application US/09948391A
Publication No. US20030027311A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                               APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.3
Matches 107, Conservative
                                                                 GENERAL INFORMATION:
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SEQ ID NO 6
LENGTH: 105
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